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SEARCH REQUEST FORM

Scientific and Technical Information Center

	Requester's Full Name: Ull 1/2 /Art Unit: 1/2 / Art Unit: Phone Nu Mail Box and Bldg/Room Location:	imber 30 ペ マタイ	Examiner #: 72967 Date: 1/29/02  Serial Number: 69/03/05  SFormat Preferred (circle): PAPER DISK E-MAIL
	If more than one search is submit	ted, please prioritize	searches in order of need.
	Please provide a detailed statement of the se Include the elected species or structures, key	earch topic, and describe as ywords, synonyms, acrony nat may have a special mea	specifically as possible the subject matter to be searched.  ns, and registry numbers, and combine with the concept or ning. Give examples or relevant citations, authors, etc., if
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	Inventors (please provide full names):	erneck,	
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	Online Time:	Other	Other (specify)

PTO-1590 (1-2000)

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AAB97366 AAM41507 AAM41789 AAM41790 AAG11577 AAG11576

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## ALIGNMENTS

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                                                                                                                                        Gordon J, Granadosen,
                                                                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                  W09856951-A1
                                                                                                                                                                                                                    LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                 LS170 polypeptide fragment.
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                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                             98WO-US11601.
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Hodges SC, Klass
Ll JC, Stroupe SD;
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                                                                                                                                       MR.
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LS170 polypeptide fragment. 29-MAR-1999 AAW95464; AAW95464 standard; peptide; 18 AA. (first entry)

LS170 gene; in vivo imaging; lung disease; cancer; drug screening.

XXXXXXX WO9856951-A1

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11-JUN-1998; 98W0-US11601

97US-00491B3

(ABBO ) ABBOTT LAB

Billing-medel PA, Cohen M, Colpitts TL, Fr: Gordon J, Granadosen, Hodges SC, Klass MR, Roberts-rapp L, Russell JC, Stroupe SD; Friedman PN; Kratochvil JD;

WPI; 1999-060335/05

New LS170 nucleic acid monitoring, preventing from lung tissue - useful for detecting, and treating lung disease, particularly

Claim 17; Page 97; 120pp; English.

Sequences AN95563-477 represent LSI70 polypeptide fragments which contain at least on epitope in thair sequences. The present invention relates to detection of starget LSI70 polymuclocide that comprises treating a test sample with any LSI70 polymuclocide that comprises that it least 50 percont identity as to me LSI70 specific nucleic acid that which are fragments derived from a thin any for the sequences (AXX0081-09) which are fragments derived from the continuous partially coveriapping sequences transcribed may be applied to the continuous partially coveriapping sequences transcribed section and transformed victor and transformed victor and transformed victor and transformed victor and partially and transformed victor and expression system complaints the LSI70 nucleic acid segmences a many transformed victor and expression system complaints the LSI70 nucleic acid segmences are made for expression system complaints. sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170-related muchaic acid can be used to isolate related sequences; as tandards and reagents in assays; as targets for drug screening, and as components or targets for therapy, e.g. antisense, ribozyme or triplex-forming can be

diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease, specifically concer, and to indicate predisposition to such disease. Particularly detection of LS170 polynucleotide, LS170 antigons, or anti-LS170 antibodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170 related nucleic acid can be used to isolate related sequences; as standards and reagents in

isolate related sequences;

and

reagents

contain at least on epitope in their sequences The present invention relates to detection of a target tail70 polynomeoride that comprises treating a test sample with at least one Lair payeefic nucleic acid that has at least 50 percent identity with any cones of LS170 sees. (AAX00801-09) nucleic acid fragments derived from various chomes of LS170 gene. The LS170 overfapping sequences transcribed from ling tissue. They are used for

Sequences AAW95463-471 represent LS170 polypeptide fragments which

Claim 17; Page 98; 120pp; English.

monitoring, New LS170 nucleic acid WPI; 1999-060335/05

preventing and

from lung tissue - useful for detecting and treating lung disease, particularly

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                                                                                                                                                          contain at least on epitope in their sequences; the present invention relates to detection of a target ISI70 polynuclectide that comprises treating a test sample with at least one ISI70 specific nucleic acid that has at least 50 percent identity with any of the sequences (AXX00801.09) which are fragments derived from various clones of ISI70 gene. The ISI70 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging prevention and treatment of lung disease. Specifically cancer, and to indicate predisposition to such disease. Particularly detection of ISI70 polynucleotide, ISI70 antibodies is indicative of disease. Cells of transformed with an expression system comprising the ISI70 nucleic acid remains a such transcribed in the composition of the compositio
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                                                                 sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS10. Tested nucleic acid can be used to isolate related sequences; as standards and reagents in assays; as targets for drug screening, and as components or targets for
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monitoring, preventing
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             therapy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can used to deliver therapeutic agents to LSI70 expressing cells; directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAW95463-471 represent LS170 polypeptide fragments which
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ussell JC, Stroupe SD;
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neutralising LS170 polypeptides);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease,
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                                                                        Sequence
                                                                                                               The present invention relates to single exon nucleic acid probes (SENP: see ANI31315-ANI57546). The present sequence is a peptide encoded by onc such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived predicting, measuring and displaying gene expression in samples derived
                                                                                                                                                                      Claim
                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #7552 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM33515;
                                                                                             human genetic disorders.
                                                                                                        rom human placenta. The probes are useful for antenatal
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nes 6; Conserv
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  1 GGGTSG 6
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                                                                                                                                                                                                                            2001-488897/53.
                                                                                                                                                                                                                                                  SG
                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful
zing gene expression in human placenta -
                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                      SEQ ID No 33784; 654pp; English
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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ilarity 100.0%;
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Pred. No.
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Pred. No.
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                               DB 22;
86;
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                                           Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                          AAM30376;
                                                                                                                                     AAM30376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000;
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mes 6; Conserv
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                                        (first entry)
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2000US-0236359.
2000GB-0024263.
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2000US-0632366.
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04-FEB-2000; 2000US-0180312
                                                  29-JAN-2001; 2001WO-US00661.
                                                                                                09-AUG-2001.
                                                                                                                                                  WO200157270-A2
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                      Peptide #4200
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inflammatory disease;

proliferative breast disease;

non-carcinoma tumour.

(first entry)

encoded by probe for measuring breast gene expression

46

51

7 gggtsg

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Query Match
Best Local
                     Matches
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                  The present invention relates to single exon nucleic acid probes (SBNP, see ANII)115-ANI5766). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                        Sequence
                                                                                                                                                                        Claim 27;
                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes analyzing gene expression in human placenta -
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26-MAY-2000;
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1 GGGTSG 6
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                                                                                             genetic disorders.
                              Similarity
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                                                                                                                                                                     SEQ ID No 30645; 654pp; English
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                                                                        93 AA;
                     Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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Pred. No.
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shes 0;
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                  Indels
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DT PRN XXX PRN
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to movel single exon nucleic acid probes (see ANIO010-ANIO067). The present sequence is a peptide encoded by one superbother the probes are useful for measuring human dene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 14258; 322pp; English.
30-DEC-1998;
02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis
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                                                                                                                                                                               W09935252-A2
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                                                                                                                             15-JUL-1999
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Conservative
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2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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98US-0222653
98US-0070346
                                                                           98WO-US27903
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                         /note= "predicted leader/signal sequence"
20..256
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 256 AA
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Pred. No. 1.6
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW95463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a novel human secreted protein, termed nysel. I The sequence is predicted from a full-length cDNA clone (see AAX59356) isolated from a human adult brain (thalamus) cDNA library. The invention provides cDNA clones (see AAX59352-58) cencoding novel secreted proteins (see AAX5946-10) of the human testis, brain and foetal kidney. The polyvuolectides and proteins are predicted to have biological activities which would make them suitable for treating preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell proliferation or differentiation, immunostimulatant (e.g. as vaccine) or immunosuppressive, haematopoies is regulating, tissue growth, activin or inhibin, chematopoies is regulating, tissue cannot support the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-419350/35
N-PSDB; AAX59356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           МсСоу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95463 standard; Protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMY ) GENETICS INST
                                   WPI; 1999-060335/05
                                                                       Roberts rapp L, Russell JC, Stroupe SD;
                                                                                             Billing-medel PA,
Gordon J, Granad
                                                                                                                                                    (ABBO ) ABBOTT
                                                                                                                                                                                              11-JUN-1997;
                                                                                                                                                                                                                                  11-JUN-1998;
                                                                                                                                                                                                                                                                           17-DEC-1998
                                                                                                                                                                                                                                                                                                               W09856951-A1
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         LS170 gene; in
                                                                                                                                                                                                                                                                                                                                                                                                                                LS170 polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW95463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cadherin or tumour invasion suppressor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGTSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merberg
                                                                                             Granadosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins-Racie LA,
                                                                                                                                                       LAB.
                                                                                                                                                                                                                                                                                                                                                                                         vivo imaging; lung disease; cancer; drug screening
                                                                                                                                                                                              97US-0049183
                                                                                                                                                                                                                                    98WO-US11601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ò
                                                                                                                 Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steininger
                                                                                             n M, Colpitts TL,
Hodges SC, Klass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                             Klass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lavallie ER;
                                                                                                                 Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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N-PSDB; AAX00809

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RESULT
AAY69164
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Best Local :
Lung specific genes for developing products for diagnosing, monitoring, staging, prognosticating, imaging and treating lung cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis stading monitoring in vivo imaging prevention and treatment of lung disease, specifically concer, and to indicate predisposition to such disease. Particularly detection of LS170 polynchectide, LS170 antigens, or anti-tS170 antibodies is indicative of disease. Cells transformed with an oxpression system comprising the LS170 nucleic acid sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening, LS170 related nucleic acid can be used to laolate related sequences; as standards and reagents in assays; as targets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or triplex founds or geners. Ab can be sthorapeutic agents (by neutralising LS170 expressing cells; directly competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
                                                                                                                                                                                                                                    04-AUG-1998;
                                                                                                                                                                                                                                                                                                                           17-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAW95463-471 represent LSI70 polypeptide fragments which contain at least on epitope in their sequences. The present invention relates to detection of a target LSI70 polypucleotide that comprises treating a test sample with at least one LSI70-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) has at least 50 percent identity with any of the sequences (AAX00801-09)
                                                                                                                                                                                                                                                                                19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                      WO200008206-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69164 standard; Protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which are fragments derived from various clones of L8170 erec. The L8170 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 96-97; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New LS170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                          2000-195589/17
DB: AAZ61165.
                                                                                                                                                                                      DIADEXUS LLC.
                                                                                                                                           Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                 98US-0095233
                                                                                                                                                                                                                                                                                99WO-US16247
                                                                                                                                        Recipon
                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung cancer; metastatic lung cancer; imaging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                           Macina RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 20;
3.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
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Example 4; SEQ ID NO 2866; 10078pp; English such as central nervous system injuries Novel nucleic acids and polypeptides,

useful

for treating disorders

WPI; 2001-442253/47. N-PSDB; AAI58877.

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AAM39721
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                         21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                           14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                Zhao
                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemostactic; chemosinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                           Tang
                                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                 19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                               26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                  W0200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is encoded by a lung specific gene, designated Logillo, clone ID 135530, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, montroring, staging or propositicating lung cancer, especially metastactic lung cancer. Antibodies against proteins encoded by lung specific genes on the used for the proteins against proteins encoded by lung specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM39721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent,
                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 35-36; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 gggtsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGTSG 6
                                                                                                              Š, į
                                                                                                                                                                HYSEQ INC
                                                                                                              Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                                                                          2000US-048B725.
2000US-052317.
2000US-059B042.
2000US-0520312.
2000US-0620312.
2000US-0653450.
2000US-0663191.
2000US-0593036.
2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; llarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                             2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                ۳,
                                                                                                                          Asundi V,
Wehrman T,
                                                                                                              Goodrich
                                                                                                              z
                                                                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA
                                                                                                            hen R, Ma Y,
Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 3.8e+02;
ches 0;
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                                                                                                                          Qian XB,
Yang Y,
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                                                                                                                                       Ren F,
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                                                                                                                                     Wang D;
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Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuties, peripheral neuropathy and localised, neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                    This invention relates to the human LUNX protein and the polynucleotide sequence encoding it. The invention includes a vector containing a LUNX polynucleotide, a host cell transformed with the vector, and an antibody polynucleotide, a host cell transformed with the vector, and an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2001078772-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUNX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human LUNX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB97366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB97366 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                       that binds to LUNX. The gene can be used for cancer diagnosis and diagnosis of micrometastatic cancer and for the production of the
                                                                                                                                                                       Claim
                                                                                                                                                                                                                       Polynucleotide encoding LUNX gene product useful for the detection cancer especially micrometastatic cancer
                                                                                                                                                                                                                                                                                                                                                                      (SAKA
                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gggtsg
product.
                                                                                                                                                                                                                                                                                                                       2001-313367/33
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                                                                                                                                                                                                                                                                                                                                                                      ) OTSUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                   especially
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6; Conser
                                                                                                                                                                                                                                                                                               AAH27756,
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ilarity 100.0%;
Conservative
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The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                          PHARM
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                                                                                                                                                                    30pp; Japanese
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Pred. No. 3.8
0; Mismatches
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   human LUNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                              LUNX
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Query Match Best Local Similarity

100.0%;

Score Pred.

33; No.

DB 22; 3.8e+02;

Length 256;

Sequence

264

Sequence

256

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AAM41507
ID AAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclorosis; Shy-Prager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening, archemokinetic; thrombolytic; drug screening, archemokinetic;
                                                                                                                                 The invention relates to human nucleic acids (AAIS798-AAI61369) and the encoded polypeptides (AAI38642-AAA42713) with mootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as peripheral nervous system diseases, such as altheimer's, Parkinson's disease. Buntington's disease, anyotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide
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25-APR-2000;
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specification
                                                   assays
                                                               lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as : Immune System suppression cathorism and activity, chemotactic/chemotachietic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao
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gggtsg
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                                                                                                                                                                                                                                                                                                                                                                           2001-442253/47.
DB; AAI60663.
                                                                                                                                                                                                                                                                                                                                          nucleic acids and
                                 disorders.
                                                 for receptor activity, arthritis
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                                                                                                                                                                                                                                                                                                                       ucleic acids and polypeptides, useful central nervous system injuries .
                                                                                                                                                                                                                                                                                        2; SEQ ID NO 6438; 10078pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu
                sequence
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0652450.
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2000US-0693936.
2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                        , z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC
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Wehrman T, X
Goodrich R,
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                  data
                  for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu C,
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                  patent
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a AJ,
RT;
                  did
                                                   and
                  not form
                                                   inflammation,
                                                                                                                                                                                                                                                                                                                                            for
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                                                                                                                                                                                                                                                                                                                                            treating disorders
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«X
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                  part of the printed
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Zhang
                                                      leukaemias
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RESULT
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Best Local S
Matches 6
The invention relates to human nucleic scids (AMI57798-AAI51369) and the encoded polypetides (AMI8642-AAM(2213) with mootropic immunosuppressant and cytostatic ectivity. The polynucleotides are useful in gene therapy. A composition containing a polypetide or polynucleotide of the invention may be used to containing a polypetide or polynucleotide system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central injuries, peripheral auropathy and altherms, such as peripheral nervous system diseases, such as localised neuropathies and central injuries system diseases, such as lateral sciences; and Shydraen, but contained the containing and shydraen other uses include the utilisation of the activity, came to such sometime system suppression, and thrombolty circ activity, came adjacents and therapy, drug screening, assays for receptor activity, arthritis and inflammantalon, leukemmias and containing assays for receptor activity, arthritis and inflammantalon, leukemmias and containing and the containing assays for receptor activity, arthritis and inflammantalon, leukemmias and containing and the containing and containing and the containing and containing
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19-OCT-2000;
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -
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Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0558042.
2000US-0508042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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ilarity 100.0%;
Conservative
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6720; 10078pp; English.
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Xu C, Xue AJ,
R, Drmanac RT;
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Pred. No. 3.9e+02;
; Mismatches 0;
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Yang Y,
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Zhang
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2000;

2000US-0727344

(HYSE-) 29-NOV

Zhao Tang

2001-442253/47. DB; AAI60946.

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Wang Z, Zhou P, HYSEQ INC

Asundi V, Wehrman T, Goodrich R,

Chen R,

Xue AJ, anac RT;

Qian XB, Yang Y,

Zhang J; Ren F,

Wang D;

Drmanac

03-AUG-2000; 14-SEP-2000; 19-OCT-2000;

19-JUL-2000;

2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000US-0620312. 2000US-0653450. 2000US-0662191. 2000US-0693036.

21-JAN-2000; 25-APR-2000; 09-JUL-2000;

26-DEC-2000;

2000WO-US34263

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM3642-AAM42213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alabehmer's, Parkinson's disease, Huntington's disease, suppreparation of the activities such as: Immune system disease, such as utilisation of the activities such as: Immune system disease.

Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -

treating disorders

2; SEQ ID NO 6721; 10078pp; English.

Example

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RESULT :
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Best Local s
Matches
                                                                                                   Human; nootropic: immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNNs; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral selerosis; SNy-Drager Syndrome; chemotacettc; chemokinettc; thrombolytic; drug sereening; arthritis; inflammation;
26-JUL-2001
                                                                                                                                                                                                                                                                                    AAM41790 standard; Protein; 272 AA
                             WO200153312-A1
                                                                                         leukaemia
                                                                                                                                                                                             Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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hybridisation assay; genetic mapping; gene expression control;
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Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                            Human heat shock protein homologue; HSPHH-1; HSPHH-2; diagnosis; cancer; inflammation; AIDS; Crohn's disease; allergy; therapy; drug screening.
                                                                                                                                                                                                                                                                                Human heat shock protein homologue 1 (HSPHH-1) protein sequence
                                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                             19-NOV-1997;
                                                                                                                                                                                                           19-NOV-1997;
                                                                                                                                                                                              97US-0974546
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                                                                                                                                                                      Shah
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New molecular chaperones useful for diagnosis, treatment of cancer and inflammation prevention and

Claim 1; Fig 1; 35pp; English.

This sequence is the human heat shock protein homologue, HSPHH-1 of the invention. The HSPHH-1 polynucleotide was isolated from the BRAITT21 CDNA library constructed from oncorous brain tissue. The HSPHH-2 DNA sequence was isolated from the BRSNNOT18 cDNA library constructed with HSPHH care useful for disparated with HSPHH care useful for disparated with HSPHH care useful for describing heads and stine and stine complements are also useful as antagonists for complements are useful for drug screening using care useful for describing the sequences and the sequences of compounds. The HSPHH-1 and HSPHH-2 nucleotide sequences and the complements, are useful for detecting upstream sequences their complements, are useful for detecting upstream sequences and their complements, are useful for detecting upstream sequences. probes.

Sequence 348

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Query Match
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                       AAB94509
               AAB94509 standard; Protein;
ААН94509;
                                                       1 GGGTSG 6
111111
75 gggtsg 80
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                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
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Pred. No.
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5e+02;
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26-JUN-2001

(first entry)

Human protein sequence SEQ ID NO:15218

Human; primer; detection; diagnosis; antisense therapy; gene therapy.

RESULT 19 AAY32858

Homo sapiens

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                                                                                                                                                                RESULT 21
AAW69428
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Best Local Similarity
Matches 6; Conserv
           Human secreted protein bp537_4
                                                                                                                                   AAW69428 standard; Protein; 378 AA
                                                          18-JAN-1999
                                                                                                   AAW69428;
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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š, Sugiyama
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This polypeptide, designated bp537_4, comprises a novel human scretced protein that is encoded by a cDNA clone (see ANV88758) and solven from a human foetal kidney cDNA library. Homology is a silvated from a human foetal kidney cDNA library. Homology is a silvated control to some database sequences. The invention provides isolated control to some database sequences. The invention provides isolated control to some database sequences. The invention provides isolated control to some database sequences. The invention provides isolated control to some database sequences. The invention provides isolated control to some database sequences. The invention and the sequence is some database sequences and set and sequences and sequences are simulating or suppressing activity, and control to the sequence is sequenced activity, and cativity, receptor. Ideal activity, and cativity, receptor. Ideal activity, and cativity, and and and cativity, and and cativity and cativity, and cativity, and cativity, and cativity, and cativity, and cativity, and and cativity and ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotides and secreted proteins - useful as, e.g
nutritional additives, immunostimulators, haemotopolesis regulators
and as diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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11-MAR-1997;
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Racie LA, Spaulding V,
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Pred. No. 5.4e+02;
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AAG12987
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Best Local
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                       AAG12987;
                                     AAG12987 standard; Protein; 499
                                                                             252 gggtsg
                                                                                              1 GGGTSG
                                                                             257
   (first entry)
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0

termination sequence hybridisation assay; genetic

Protein identification; signal transduction pathway; metabolic pathway;

mapping; gene expression control; promoter;

Arabidopsis thaliana protein fragment SEQ ID NO:

Arabidopsis thaliana

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				99US-011019 99US-0110449 99US-0110510 99US-0110510 99US-0110491 99US-0112048 99US-0112048 99US-0112444 99US-0112446 99US-0112465 99US-0112465 99US-0112467 99US-0112467	
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                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway: metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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6; Conserv
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ilarity 100.0%;
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                99US-0121825.
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RESULT AAB93590 (AAB93590 AAB93590 AAB9360 AAB940 A
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11-JAN-2000;
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WPI; 2001-318749/34
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                                              Isogai T, Nishikawa T, Sugiyama T, Wakamats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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ilarity 100.0%;
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                                                                                                                              INST
                                                  Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO:13016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520
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Pred. No.
                                                  Hayashi K,
1 A, Nagai F
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                                                  Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
6.9e+02;
                                                                           Saito K,
                                                      Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention describes primer sets for synthesising 5602 (full-length cDNAs defined in the specification. Where a primer set (c) comprises: (a) an oligo-dr primer set (c) the comprises: (a) an oligo-dr primer and an oligo-nucleotide complementary to the 500 nucleotide sequences defined in the specification, where the coligonucleotide sequences defined in the specification, where the coligonucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises a 5-end complementary to the complementary to the complementary strand of a polynucleotide which comprises a 5-end complementary to a complementary to a complementary to a complementary to the comprises a 3-end sequence complementary to a complementary t
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06-APR-1999
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                                                                                                                                                                                                                                             06;SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
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501 gggtsg 506
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                                                                                                                                                                                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                        termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 552
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Pred. No. 7.1e+02;
Mismatches 0;
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hybridisation assay; gentermination sequence.
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Pred. No. 7.5
); Mismatches
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7.5e+02;
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expression control;
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promoter;
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19-JUL-1999
20-JUL-1999
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RESULT :
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22-0CT 1999
22-0CT 1999
25-0CT 1999
25-0CT 1999
25-0CT 1999
26-0CT 1999
                                                                                                                                                                                        27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNs defined in the specification. Where a primer set comprises: (a) an oilgo-dT primer and an oilgonucleotide comprises to the complementary strand of a polynucleotide which comprises one of
                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                  Ota T,
Ishii
                                                                                                                                            Ota
                                                                                                                                                                                                                                                          07-FEB-2001
                                                Claim
                                                                                                               WPI; 2001-318749/34.
                                                                                                                                                             (HELI-)
                                                                                                                                                                                09-JUN-2000;
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                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                 Human;
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6; Conserv
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Sugiyama
                                               SEQ ID 14452;
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2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                   sequence
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9903-0160980
9903-0160980
9903-016406
9903-016406
9903-016406
9903-016406
9903-0164350
9903-0164350
9903-0164350
9903-0164350
9903-0164920
9903-0164920
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99US-0160767.
99US-0160768.
                                                                                                                                                                                                                                                                                                              detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                     99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9908-0162142
                                                                                                                                Nishikawa T,
T, Wakamatsı
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                                              2537pp +
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Pred. No. 7.5e+02;
                                               CD ROM; English
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                                                                                                                                Hayashi K,
A, Nagai
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                                                                                                                                Saito K,
Otsuki
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encoded by the
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                                                                                                                                          Yamamoto
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AAG81993
                                             RESULT
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 5002 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of 1500 nucleotide comprises at least 15 nucleotides and the combination of 1500 nucleotides and the 1500 nucleotides and 1500 nucleotides nucleotides and 1500 nucleotides nucleotide
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6; Conserv
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nilarity 100.
Conservative
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Pred. No.
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.6e+02;
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03-SEP-2001
                                                                            AAG81993 standard; Protein; 582 AA
                                       AAG81993;
(first entry)
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epidermidis open reading frame protein sequence SEQ ID NO:1080

Staphylococcus Staphylococcus epidermidis endocarditis epidermidis SR1 strain; infection; diagnosis;

WO200134809-A2

17-MAY-2001

09-NOV-1999; 09-NOV-2000; 2000WO-US30782 99US-0164258

(GLAX ) GLAXO GROUP LTD.

Kimmerly ξ

2001-316495/33. )B; AAH52843.

Nucleic acids encoding useful for vaccinating polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis

Claim 18; Page 315; 2188pp; English.

(II), given in AAGBIASA to ANNUALLY CITY and therefore can be used. I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors s. epidermidis polypeptides (II) via the production of vectors of the value o AAH53970 represent nucleic acids (I) encoding in AAG81454 to AAG83120, from Staphylococcus encoding polypeptides
lococcus epidermidis.
therefore can be used be the

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Query Match
Best Local :
Matches
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, nootropic; immunosuppressant; cycostatic; gene therapy; cancer; peripheral nervous system; cancepathy; central nervous system; cancepathy; central nervous system; cancepathy; central nervous system; cancepathy; central nervous system; charcostatic; amyotrophic lateral sciencesis; Shy Danger syndrome; charcotrotic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to vaccinate subjects and to raise antibodies against the bacteria. The polyapetides may also be used to assay for other inhibitors of their activity and therefore identify componing for other inhibitors of their treatment of s. epidemids infections: 3. g. identify the used for the AMIS5090 represent specifically claims: 3. g. identify spendic DNA polyanciactide sequences from the assent invention specifically claims of the present invention. AMIS5091 to AMIS5098 represent oligonucleotide sequences from the assent invention process which are used in the assent invention specification of the present than plants specification of the present specification specification in the sequence listing of the present polyanciactide sequences given in the sequence listing only socially 100:455 so even though sequences are given in the discharge for ID NO:465 to 4472, no sequences are given in the discharge for ID NO:465 to 4472.
   Example 4; SEQ
                                          Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 3149.
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                                                                                                                                                                                                                                                                      (HYSE-)
                                                                                                                                                                                                                                                                                                                   29-NOV-2000;
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DB; AAI59160.
                                                                                                                                                                          Wang z,
zhou P,
                                                                                                                                                                                                                                                                      HYSEQ
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6; Conserver
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2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-062312.
2000US-0653450.
2000US-0663191.
2000US-06393036.
2000US-0727344.
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Wehrman T,
Goodrich F
   ð
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3149; 10078pp; English
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Pred. No.
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Ku C, Xue AJ,
Drmanac RT;
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ches 0;
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Yang Y,
                                                                for
                                                            treating disorders
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Zhang
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RESULT .
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Best Local
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25-APR-2000;
09-JUL-2000;
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           WPI; 2001-442253/47
N-PSDB; AAI59159.
                                                               Tang
                                                      Zhao
                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                             19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                   26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        chemokinetic; thrombolytic; drug screening; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy, central nervous system; CNS,
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatlo;
amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactlo;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                                                    19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                             Leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification.
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                                                    P, T
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                                                    Liu C
Wang Z
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
6; Conserv
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                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-05588042.
2000US-0620312.
2000US-06520312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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                                                u C,
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                                                  Asundi V, Cl
Wehrman T, 1
Goodrich R,
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                                                                 Chen R,
Xu C,
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Pred. No.
                                                    Drmanac
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                                                               Xue AJ,
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                                                               y, δ
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                                                               Ren F,
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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AAB94603
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Best Local S
Matches (
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAIS7798-AAIS1369) and the encoded polypeptides (AAIS462-AAMA213) with noutropic. I mamunosuppressant and cytostatic activity The plyvacionides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous properties, and control nervous system places. Such and localised neuropathies and central nervous system places. Such and labeliner's, parkinson's disease, Huntington's disease, such alternal sclerosis, and Shy-Dager Syndrome. Other issee, amorrophic utilisation of the activities will be such as Immuno system places them. Statistically, chambas and the properties are properties and the properties are properties.
                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                       11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein
                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB94603 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 gggtsg 111
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mes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                     Isogai T,
                                                                                                                                                                                       Sugiyama
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                                                                                                                                                                                                                                                                                                                     99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence SEQ ID NO:15428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                   Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 678 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 22;
Pred. No. 8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                   Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                   Saito K, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                              Yamamoto
                   detection
by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Ceffull-length cDNAs defined in the specification where a primer set for synthesising 5602 ceffull-length cDNAs defined in the specification where a primer set comprises; (a) an oligo-df primer and an oligonucleothide complementary to the complementary strond of a polynucleothide complementary strond of a polynucleothide comprises one of ceffund in the tips of the complementary strond of a polynucleothide; or the complementary complementary is not between the complementary complementary at the complementary at the complementary as the complementary strond of a polynucleothide which phenomenary complementary to a complementary strond of a polynucleothide which comprises a cequence complementary to a complementary strond of a polynucleothide which comprises a least 15 nucleothide which complementary to a complementary strond of a polynucleothide comprision a sequence complementary to a complementary strond of a polynucleothide comprises a least 15 nucleothide complementary to a complementary to a complementary strong complementary to a compleme
      Sequence
                                                                                    the present invention.
678 AA;
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Matches
                                           Query Match
Best Local
659 gggtsg 664
                                           Local Similarity
                 1 GGGTSG 6
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                                  100.0%;
ilarity 100.0%;
Conservative (
                                  0
                                           Score 33;
Pred. No.
                                  Mismatches
                                         9e+02;
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                                  Indels
                                 0;
                               Gaps
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DB 22;

Length 678;

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RESULT

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AAY84686
  08-AUG-2000
                                                      AAY84686 standard; Protein; 2071 AA
                                                                                    32
(first entry)
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Amino acid sequence of AC003, a GTPase activating protein.

phosphatidylinositol-4 kinase; cytokenesis gene; fungicidal; filamentous fungi; plant pathogen; se GTP-binding protein; AG003; GTPase activating protein; fungal growth; septoria tritici;

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Stagnospora nodorum; Magnaporthe grisea; human pathogen; Candida albicans; Aspergillus fumigatus.
Aspergillus
fumigatus
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20-APR-2000
                            WO200022133-A1
                                                        Ashbya gossypii.
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(NOVS) NOVARTIS AG. NOVARTIS-ERFINDUNGEN VERW GES

08-OCT-1998; 06-OCT-1999;

98US-0168804 99WO-EP07501

TD, Wendland Ç Dietrich F, Philippsen P, Goff

DT CONTRACTOR OF THE CONTRACTO WPI; 2000-317988/27 N-PSDB; AAA14503.

Ashbya gossypli nucleotide and protein sequences useful for identifying fungal growth inhibitors  $\,\cdot\,$ 

Claim 8; SEQ ID 15428; 2537pp + CD

ROM; English

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AAB86196
ID AAB
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein gene, and a putative cytokenesis gene. These genes are essential for fungal growth and development. The proteins can be used in methods to identify compounds that have fungicialal activity. Compounds with fungicidal activity can be used for suppressing fungal growth, especially of filamentous fungi. Fungi that can be suppressed include plant pathogens (e.g. Septoria tritici, Stagnospora modorum, and Mannaporthe grisea) and human pathogens (e.g. Candida albicans, and Aspergillus fumigatus).
This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C.6" which can be used for the induction of specific humoral and cellular immune responses. (1) and polypeptides (II) encoded by them, are useful in pharmaceuticals, vaccines and disgnostic agents, particularly for treatment or prevention of human immune deficiency virus-1 (HIV-1) infections, also for rational
                                                                                        Disclosure;
                                                                                                                         New nucleic acid sequences from a human immune intersubtype, useful for treatment, prevention
                                                                                                                                                                  WPI; 2001-336417/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB86196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB86196 standard; Protein; 3025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                             16-NOV-2000;
                                                                                                                                                                                                                                                                                                      31-MAY-2001
                                                                                                                                                                                                                                                                                                                            DE10056747-A1
                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 subtype C protein fragment #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence
                                                                                                                                                                                                                             (SHAO/)
                                                                                                                                                                                                                                                     16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infection;
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                                                                                                                                                                                                                                                                                                                                                                                                               immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conserv
                                                                                                                                                                                                               GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG
                                                                                                                                                                                                                             SHAO Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein genes, putative phosphatidylinositol-4 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 48-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1mmune
                                                                                                                                                                                       Wolf H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2071 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                        Fig 8A-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                             2000DE-1056747
                                                                                                                                                                                                                                                     99DE-1055089
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         response;
                                                                                                                                                                                                                                                                                                                                                      note-
                                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification also describes putative GTP enes, putative showshertanding.
                                                                                                                                                                                       Shao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93pp;
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                                                                                    48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       human;
                                                                                                                                                                                                                                                                                                                                                   "Xaa
                                                                                                                                                                                                                                                                                                                                                                Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                        German
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                                                                                                                                                                                                                                                                                                                                                    represents a stop codon'
                                                                                                                                                                                         Graf
                                                                                                                                                                                                                                                                                                                                                                                                                                                     humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                         x
                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4e+03;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
                                                                                                                          deficiency virus
and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2071;
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1 GGGTSG

Query Match Best Local Matches

Similarity 5; Conser

Conservative

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Mismatches

Indels 32;

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Score 30; Pred. No.

1.8e+02

DΒ

20;

Length

Match

Sequence

32

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low-phenylalanine diets

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RESULT 34
AAW90042
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                        of a phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. M4. The encoding pdh nucleic acid is used to produce recombinant Rhodococcus L-phenylalanine dehydrogenase, which can be used to produce L-amino acids from the corresponding alpha-keto acids, e.g. to produce L-phenylalanine from phenylpyruvic acid (e.g. for the production of aspartame), to screen for phenylaktonuria in newborn infants and to monitor the efficacy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    design of test or therapeutic reagents, or gene therapy vectors. Polypopildes, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and dispositic against (II) are specially useful as pharmaceutical and dispositic agains of special to the intersubtype C/B of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent the products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in
                                                                                                                                                                 Disclosure; Fig 4; 30pp; English
                                                                                                                                                                                               DNA encoding Rhodococcus L-phenylalanine dehydrogenase - production of recombinant enzyme
                                                                                                                                                                                                                                           WPI; 1999-080406/07
                                                                                                                                                                                                                                                                         Blanchard
                                                                                                                                                                                                                                                                                                                                    05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aspartame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. stearothermophilus alanine dehydrogenase fragment #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW90042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW90042 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2639 gggtsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                    (YESH ) UNIV YESHIVA EINSTEIN COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGTSG
                                                                                                                                   sequence is used to describe a method which results in the isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production; phenylketonuria; infant; alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase; pdh; L-amino acid; phenylpyruvic acid;
duction; phenylketonuria; infant; alanine dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                                                                                                  95US-0461990
                                                                                                                                                                                                                                                                                                                                                                95US-0461990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
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                                                                                                                      This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antinicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 228; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences from Staphylococcus aureus WCHU29 useful in vaccines and for treatment of bacterial infections
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N-PSDB; AAV53319.
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Lonetto MA,
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Phenylalanine dehydrogenase; pdh; L-amino acid; phenylpyruvic acid; aspartame production; phenylketonuria; infant; alanine dehydrogenase; diet.
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DNA encoding Rhodococcus L-phenylalanine dehydrogenase production of recombinant enzyme

This sequence is used to describe a method which results in the isolation of a phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. 44. The encoding pdh nucleic acid is used to produce recombinant Rhodococcus (-phenylalanine dehydrogenase, which can be used to produce L-minno acids from the corresponding alpha-kec acids, e.g. to produce L-minno acids from phenylpyruvic acid (e.g. for the production of aspartame), to screen for phenylatonuria in newborn infants and to monitor the efficacy of low-phenylalanine diets.

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Length 95
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protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; pathway;
promoter;

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1; Mismatches 0
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                                                        YL55_CAEEL
NRDI_ECOLI
YJF5_CAEEL
YJF5_THMAN
IF31_HUMAN
EUTJ_ECOLI
EUTJ_ECOLI
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OTX3_BRARE
MURG_STRCU
                                                                                         KF3C_RAT
CLAB_LYCES
CLAA_LYCES
YL55_CAEEL
NRDI_ECOLI
YJF5_YEAST
                                                                                                                             K2C3_HUMAN
UL52_HCMVA
SP87_DICDI
NH48_CAEEL
KF3C_RAT
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CDX4_HUMAN
MDL1_PRUDU
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PTLB_LACLA
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ZIC2_HUMAN
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RBL2_CHRVI
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LORI_MOUSE
Y136_TREPA
CDSN_HUMAN
GATC_DROME
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VAOD_NEUCR
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SERC\_YEAST DDL\_TREPA MURG\_MYCLE

RESULT

ALIGNMENTS

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DT 15-JUL
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DE COX4.93
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Matches 6
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15-JUL-1998
30-MAY-2000
                                                                                                      Footes M.;

"Genomic structure of the human CDX4 gene: a potential c
the FG syndrome.";

Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Chen E.Y., States D.J.,
Submitted (MAY-1997) to
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O14627;
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                                                                                                                                                                                                                                                           Chiaroni
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Mammalia; Eutherla; Primates;
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PIR; X07509; S00739;
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*Nucleotide sequence of regions homologous to nifH (nitrogenase protein) from the nitrogen-fixing archaebacteria Methanococcus thermolithotrophicus and Methanobacterium Ivanovil: evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus thermolithotrophicus.
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01-NOV-1988 (Rel. 10, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL PROTEIN IN NIFH2 3' REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embry Spermatophyta; Magnollophyta; eudtoctyledons; eurosids I; Rosales; Rosaceae Drown Prunus dulcis (Almond) (Prunus amygdalus). Embryophyta; Tracheophyta; edons; core eudicots; Rosid

Rosidae;

Submitted (SEP-1995) to the EMBL/GenBark/DDBJ databases
-- FUNCTION: INVOLVED IN CYANGGENIS, THE RELEASE OF HCN FROM INJURED
-- FUNCTION: INVOLVED IN CYANGGENIS, THE RELEASE OF HCN TO A VARIETY
OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN (BY

Suelves STRAIN-CV. TEXAS; SEQUENCE FROM N.A.

TISSUE-Flower;

SIMILARITY). MANDELONITRILE - CYANIDE + BENZALI COPACTOR: FAD (BY SIMILARITY). SUBUNIT: MONDER (BY SIMILARITY). SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY BENZALDEHYDE

the This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics by non-profit institu s Institute. The There are no restrictions 9 1ts

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15-DEC-1998 (Rel. 3
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                          "Immunocytochemical localization of mandelonitrile black cherry (Frunus serotina Ehrh.) seeds."; plant Physiol. 96:1239-137(1991).
                                                                                                                     Wu H.-C.,
                                                                                                                                                                                                                                       Hu Z.,
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Plant Cell
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                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                   identification of a
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                                                                                                                                               FISSUE-Seed;
                                                                                                                                                                   SEQUENCE
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TE; PS00623; GMC_OXRED_1;
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                                                                                                                     Poulton J.
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                MEDLINE-91093107; pubMed-2125052; de Vos W.M., Boerrigter I.J., van Hengstenberg W.; "Characterization of the lactose-
                                                                                                                                                                                                                                                                                                                                                                                                                             LACLA
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heen the Swiss Institute of Bhoinformatics and the ED
European Bioinformatics Institute. There are no rest
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SUBCELLULAR LOCATION:
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OF ENZYME INCREASES WITH SPECIFICITY FOR
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FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOEMOLPYRUVATE-DEPENDENT SUCAR PROSPHOFANSE ESSEME (PTS). MAJOR CARBOHIDRATE ACTIVE TRANSPORT SYSTEM, THE LICE DOMAIN THE SUCAR BINDING SITE TO AND THE TRANSPORT SYSTEM, THE LICE DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DOMOI IS PHOSPHORYLATION SITE THE DOMOI IS PHOSPHORYLATION SITE THE DOMOI IS PHOSPHORYLATION SITE TO THE DOMOI IS PHOSPHORYLATION SITE OF THE P

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CATALUTIC ACTIVITY: PROTEIN N-PHOSEPHOHISTIDINE + PROTEIN HISTIDINE + SUGAR PROSEPHOHISTIDINE + SUBCELLULAR LOCATION INTEGRAL MEMBRARE PROTEIN. SIHILARITY: CONTAINS A PTS EIIE DOMAIN.
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Hoinformatics and the EMHo quietation to European Bioinformatics institute. There are no restrictions on its European Bioinformatics institute, There are no restrictions on its European Bioinformatics institutions as long as its content is in no way by non-profit institutions as long as its content is in no way

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Pfam; PF02302; PTS_IIB; 1.
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InterPro; IPR003352; PTS_EIIC.
InterPro; IPR003501; PTS_IIB.
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LACTOSE-SPECIFIC IIBC COMPONENT (
BE COMPONENT) (PHOSPHOTRANSFERASE
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*Nucleotide and deduced maino acid sequences of the lack, lackBCD,
and lacFE dense encoding the repressor, teaguese 6 phosphate gene
cluster, and augur-specific phosphotransfeagatese system components o
the lactose operon of Streptococcus mutans.";
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MEDLINE-94103744; PubMed-8277252;
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STRAIN-UA130 / SEROTYPE C;
MEDLINE-93015655; PubMed-1400164;
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InterPro; IPR003501; PTS_IIB.
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CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE +
PROTEIN HISTIDINE + SUGAR PHOSPHATE.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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POTENTIAL.
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Best Local
   P24400;
01-MAR-1992
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PTS SYSTEM,
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NCBI_TaxID=1280;
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01-JUN-1994 (Rel. 29, Last annotation update)
PTS SYSTEM, LACTOSE-SPECIFIC ING CONPONENT (EIIBC-LAC)
PERMEASE (INC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II,
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Phosphotransferase system; Sugar transport;
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Interpro; IPR003352; PTS_EIIC.
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J. Biol. Chem.
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MEDLINE-88059023; PubMed-2824493;
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BC COMPONENT)
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RESULT . 9
GCKR\_HUMAN

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485 GGGTSG

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                       Matches
                                 Query Match
Best Local
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                                                                                                                  TRANSMEM
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TRANSMEM
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TRANSMEM
                                                                                 SEQUENCE
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                          Phosphorylation;
                                                                                                                                                                                                                                                                          Phosphotransferase
                                                                                                                                                                                                                                                                                    Pfam; PF02378; PTS_EIIC; 1
Pfam; PF02302; PTS_IIB; 1.
                                                                                                                                                                                                                                                                                                             InterPro; IPR003352;
InterPro; IPR003501;
                                                                                                                                                                                                                                                                                                                                    EMBL; M60851; AAA72984.1; -. PIR; B23697; B23697.
                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "wholecular cloning and DNA sequence of lacE, the gene encoding lactose-specific enzyme II of the phosphotransferase system of Lactobacillus case!. Byidence that a cysteine residue is essen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpert C.-A., Chassy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-91093108; PubMed-2125053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMEASE IIBC COMPONENT) (EC 2.7.1.69) (EII-LAC).
                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus casei
                                                                                                        TRANSMEN
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1 GGGTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE SUGAR.

CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE PROTEIN HISTIDINE + SUGAR PHOSPHATE.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUGAR PROSEBOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHUDANTE ACTIVE
"TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
HOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HER); ITA TRANSFERS ITS
HOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HER); ITA TRANSFERS ITS
HOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HER); TA TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIOI. Chem. 265:22561-22568(1990).
FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
                       Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Firmicutes;
 6
                        Conservative
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100
133
176
219
2280
326
363
386
4286
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                                                                                                                                                                                                                                                               Transmembrane
                                                                                                      577
47
83
120
153
153
196
239
300
346
448
                                                                                                                                                                                                                                                                          system;
                                                                                                                                                                                                                                                                                                           PTS_EIIC.
                                                                                 62391
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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BE56852CAB0D76E4 CRC64;
                                 Pred. No.
                                                                                                                                                                                                                                       BIIB
                                                                                                                                                                                                                            POTENTIAL
                        Mismatches
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   It is produced through a collaboration
                                                DB 1;
                                  .1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME
                                              Length
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                                                                                                   RESULT
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Best Local S
Matches
                GCKR_RAT
Q07071;
Q1-OCT-1994
Q1-FEB-1995
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCKR_HUMAN STANDARD.
Q1497; Q9952;
01-NOV-1997 (Rel 35, CI
30-MAY-2000 (Rel 39, LI
20-AUG-2001 (Rel 40, LI
GLUCOKINASE REGULATORY);
GCKR.
     GLUCOKINASE
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z48475; CAA88367.1; -. EMBL; Y09593; CAA70779.2; -. EMBL; Y09592; CAB61828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit Lantitutions as long ass its content is in modified and this statement is not removed. Usage by and for to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCLE, BRAIN, HEARY, THYMUS, INTESTINE, UTERUS, ADIPH
KIDNEY, ADRENAL, LUNG OR SPLEEN,
-1- SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBPANILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- TISSUE SPECIFICITY: FOUND MUSCLE, BRAIN, HEART, THYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marner J.P., Bonthron D.T.;

**Organization of the human glucokinase regulator gene GCKR.*;

Genomics 49:137-147(198).

**IP FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A., REVISIONS, AND VARIANT LEU-446
MEDLLNE-98234554; Pubmed-9570959;
Hayward B.E., Dunlop N., Intody S., Leek J.P., Markham A.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Human glucokinase regulatory protein (GCKR): Bonthron D.T.;
*Human glucokinase regulatory protein (GCKR): cDNA and genomic
cloning, complete primary structure, and chromosomal localization.*;
Mamm. Genome 6:532-536(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                       Polymorphism.
                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                             Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001741; GCKR
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                      MIM; 600842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96014291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                        106 GGGTSG
                                                                                                                                                                                               Local Similarity
les 6; Conser
                                                                                                                                                                  1 GGGTSG
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                                                                                                                                                                                                                                                                                                                   PD025295; GCKR; 1.
; PS01272; GCKR; 1.
                                                                                                                                                                                                                                                                625
(Rel. 30, Created)
(Rel. 31, Last sequence update)
(Rel. 39, Last annotation update)
REGULATORY PROTEIN (GLUCOKINASE REGULATOR).
                                                                                                                                          111
                                                                                                                                                                  6
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                          446
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Leek J.P., Intody S.
                                                                                                                                                                                                                                                                Š
                                                                     STANDARD;
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. 39, Last sequence upd
.. 40, Last annotation U
LATORY PROTEIN (GLUCOK)
                                                                                                                                                                                                                                                                                          446
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Primates;
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Pred. No.
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DE750462AC603C80 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLUCOKINASE
                                                                                                                                                                                           red. No. 1.2e+02;
Mismatches 0;
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                                                                                                                                                                                                                     Length 625;
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K2C3_HUMAN
ID K2C3_HUMAN
AC P12035;
DT 01-OCT-1989
          SOFT REAL PROCESS OF THE PROCESS OF 
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Best Local
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InterPro: IPRO01741; GCXR
InterPro: IPRO01347; SIS:
Pfam: PF01390; SIS: 1.
ProDom: PF003595; GCKR; 1.
PROSTIE: PF01272; GCKR; 1.
Kilinge E.M., Sylvestre Y.R., Freedberg I.M., Blumenberg "Boolution of keratin genes: different protein domains different pathways.":
                                                                              SEQUENCE FROM N.A. MEDILINE-87254239; PubMed-2439698;
                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                          CYTOKERATIN).
                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1987 (Rel. 40, Last anotation update)
CERATIN, TYPE II CYTOSKELETAL 3 (CYTOKERATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BWEL outstation. The Buropean Bloinformatics Institute of Bloinformatics are no restrictions on its use by non-profit institutions as long and its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein of glucokinase.";
FEBS Lett. 339:312-312(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS
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"Cloning and sequencing of rat liver cDNAs encoding the regulatory
morain of dimokinase.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94156054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93238935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGTSG
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SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
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Lett. 321:111-115(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626
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Llarity 100.0%;
Conservative (
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                                                                                                                                                                               Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33;
Pred. No.
                                                                                                                                                                               Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60A6A57FBACD1FF3 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  red. No. 1.2e+02;
Mismatches 0;
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                                                                                                                                                                                                           Vertebrata;
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EMBL: X05419; CAN28992.1; AIT_SEQ.
EMBL: X05420; CAN28993.1; AIT_SEQ.
EMBL: X05420; CAN28994.1; AIT_SEQ.
EMBL: X05420; CAN28994.1; AIT_SEQ.
EMBL: X05421; CAN28996.1; AIT_SEQ.
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PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR003054; Keratin_II.
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the European Bioinformatics institute. There are no rest
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Nat. Genet. 16:184-187(1997).
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"Mutations in cornea-specific keratin K3 or K12 genes cause
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E -> K (IN MCD).
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Pred. No. 1.2e+02;
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SEQUENCE
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CHERT TOP. Microbiol. Immunol. 154:125-169(1990).

1- SHMILARITY: BELONGS TO FRANLY THAT GROUPS TOGETHER HSV-1 UL32, EHV-1 28, EBV BFLF1, HCMV UL52, AND VZV 26.
STRAIN-AX3;
MEDLINE-94229358;
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                                                   SEQUENCE FROM N.A
                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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MEDLINE=90269039; PubMed=2161319;
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MCBI_TaxID=10360;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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PROBABLE MAJOR ENVELOPE GLYCOPROTEIN UL52 (HFRE1 PROTEIN).
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HSSP; P06620; lina.
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ELECTRON-DENSE, PROTEINACEOUS LAYER,
SUBCELLULAR LOCATION: ACCUMULATES SPECIFICALLY IN REGULAT
SECRETORY VESICLES OF PRESPORE CELLS (PRESPORE VESTCLES),
PROTEIN LATER ACCUMULATES EXTRACELLULARLY IN THE SPORE CO
INDUCTION: BY C-MP.
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NH48_CAEEL
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Best Local
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                               KF3C_BAT STANDARD;
O55165; O88657;
15-DEC-1998 (Rel. 37, Create
15-DEC-1998 (Rel. 37, Last t
20-AUG-2001 (Rel. 40, Last t
KINESIN-LIKE PROTEIN KIF3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NH48_CAEEL
Q94407;
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                            DNA_BIND
ZN_FING
ZN_FING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00105; zf-C4; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z79604; CAB01900.1;
HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHR-48 OR ZK662.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last annotation update) NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-48
Rattus norvegicus (
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                          Receptor; Transcription regulation; Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                               WormPep; ZK662.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1996)
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                        KIF3C
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                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR001628; zf-C4.
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Similarity 100.0%;
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(Rat).
a; Chordata;
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tive 0; Mismatches 0;
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C4-TYPE.
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Pred. No. 1.5e+02;
Craniata; Vertebrata; Euteleostomi;
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Best Local
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P31542;
01-JUL-1993
01-JUL-1993
01-FEB-1996
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CONFLICT
SEQUENCE
Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplante; Steptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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DOMAIN
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NP_BIND
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                                                                                                                                                 CD4B.
                                                                                                                                                                            ATP-DEPENDENT
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ223599; CAA11465.1; --
EMBL; AF083330; AAC33291.1; --
InterPro; IPR001752; kinesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associates with membrane vesicles.", Mol. Biol. Cell 9:637-652(1998).
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*KIF3C and KIF3A form a novel neuronal heteromeric kinesin that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muresan V., Abramson T.,
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NCBI_TaxID=10116;
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SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
II SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES.
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6; Conserv
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oceli: Microtubules Affr-binding; Coiled coil; Neurone.

of Affr-binding; Coiled coil; Neurone.

secunocal (Motor) (BY SIMILARITY).

378 632 COILED COIL (POTENTAL).
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(Rel.
NT CLP
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                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                         26, Created)
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PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B
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POLY-PRO.
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POLY-GLY.
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Pred. No.
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1.6e+02;
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    MEDLINE-90239044; PubMed-2185473;
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                                                  Lycopersicon esculentum (Tomato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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MAILICK J.S., Dallympile B., Kuranitsu H., Shiroza T., Foster J.
Clark M., Ross B., Squifes C.L., Mauriti M.R.,
"Conservation of the squiatory subunit to the Clp ATP-depend
protease in prokaryotes and enkaryotes for protease in prokaryotes and enkaryotes for SJ71(1990).
PROC. NALL ACAD. SCI. U.S.A. BF.3513-3577(1990).
SEQUENCE FROM N.A
                                        NCBI_TaxID=4081;
                                                                                                                                                        PRECURSOR.
                                                                                                                                                                        ATP-DEPENDENT
                                                                                                                                                                                                                                                      CLAA_LYCES
P31541;
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TRANSIT
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PROSITE; PS00871; CLPAB_2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
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use by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                   244 GGGTSG
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ATP-binding; Repeat; Chloroplast; Transit peptide.
ATP-DEPENDENT CLP PROTENSE ATP-BINDING
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Conservative
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NT CLP PROTEASE ATP-BINDING SUBUNIT
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P34435;
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01-FEB-1994
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SEQUENCE
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"Conservation of the regulatory submit for the Clp Arp-depend processe in profaryoles and subarryoles. Sin Proc. Natural Conference of the Clp Arp-depend processe in profaryoles and subarryoles. Sin (1990).

Proc. Natural Natural Conference of the Cut Archive Development of the Cut Archive De
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2.
MEDLINE-94150718; PubMed-7906398;
Wilson R., Ainscough R., Anderson
Bonfield J., Burton J., Connell M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00359; AAA.
InterPro; IPR001399; AAA_subfam.
InterPro; IPR001270; CLP_AB.
InterPro; IPR001343; UVR.
Pfam; PF0004; AAA. 2.
Pfam; PF02151; UVR; 1.
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or send an emall to license@isb-sib.ch).
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                                                                                                                                                                                                                      HYPOTHETICAL
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                                                                                                                Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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SM00382; AAA; 2.
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. PROTEIN F44E2.5 IN CHROMOSOME
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  Connell M.,
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                      Anderson K.,
                                                                                                                                            Caenorhabditis
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ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOWOLGG CDAA.
2 x 32 AA APPROXIMATE REPEATS.
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Pred. No. 1.8e+02;
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Copsey T.,
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  Cooper J.,
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RESULT NRDI\_EC

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update) 136

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NRDI PROTEIN.
NRDI OR B2674 OR Z3976 OR
Escherichia coli, and
Escherichia coli 0157:H7.

Escherichia

NCBI\_TaxID=562,

Bacteria; Proteobacteria;

gamma subdivision; Enterobacteriaceae;

RECENT REPAY OF THE PROPERTY O

STRAIN=K12; MEDLINE=97349980;

PubMed-9205837

SEQUENCE FROM N.A.

"The complete genome sequence Science 277:1453-1474(1997). Gregor J., Davis N.W.,

of.

Escherichia coli K-12.";

B., Shao Y.;

Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., Ro Gregor J., Davis N.W., Kirkpatrick H.A., Goo

Rode

C.K., Mayhew G. n M.A., Rose D.J

Perna N.T.,

STRAIN-K12 SEQUENCE FROM N.A

MEDLINE-97426617; PubMed-9278503;

/ MG1655;

Jordan A., Aragall E., Gibert I., Barbe J.;

"Promoter identification and expression analysis of Salmonella typhimurium and Escherichia coli nrdEF operons encoding one of class I ribonucleotide reductases present in both bacteria.", Mol. Microbiol. 19:777-790(1956).

MEDLINE-96417857; PubMed-8820648;

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Johnston L. Jones M., Kershow J., Kirsten J., Lalsater N.
Latreille J., Lalshining J., Lloyd C., Mortimore B., O'Callaghan M.,
Latreille J., Lalshining J., Lloyd C., Mortimore B., O'Callaghan M.,
Latreille J., Farery C., Lattiken L., Boopra A., Saunders D., Shownkeen
Sims H., Smith M., Smith M., Sonihammer E., Shownkeen
Sulston J., Thierry Hieg J., Thomas K., Valdin M., Valghan K.,
Waterson R., Matson A., Welistock L., Wilkinson-Sproat J.,
Waterson R., Water M., Water M., Wilkinson-Sproat J.,
Waterson R., Water M., Wellsche M., Wilkinson-Sproat J.,
Water M., Water M., Water M., Water M., Water M., Wilkinson-Sproat J.,
Water M., Water
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Pred. No. 21;
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ns T., Hillier L.,
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the European Bioinformatics institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi K., Murata T., Tanaka M., Tobe T.,
11da T., Takani H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiha T., Hattori M., Shinagwa H.;
"Complete genomic sequence of enterohemorrhagic Escherichia coli
0157.H7 and genomic comparison with a laboratory strain K-12.;
DMA Res. B.11-22(2001).
                                                                                                                                                                                                                                                                                                                                                   EMBL; D90891; BAA16538.1; ALT_INIT EMBL; AE005496; AAG57784.1; EMBL; AP002562; BAB36960.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X79787; CAA56185.1; -
EMBL; AE000352; AAC75721.1;
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STRAIN-0157:H7 / I
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Nature 409:529-533(2001).
[5]
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MEDLINE=21074935; PubMed=11206551;
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Yamagata S., Horiuchi T.;
"Construction of a contiguous 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizobuchi K., Mori H., Nake
Oshima T., Oyama S., Saito
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PF02555; NrdI; 1.
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Kimura S., Kitagawa
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togowa M., Mekino K., Miki T., Mitsihashi N.,
Nakade S., Nakamira Y., Nashimoto H.,
Nakade S., Nakamira Y., Nashimoto H.,
Sabato N., Sompei G., Sato N., Sivasundaram S.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; ATP-binding
NP_BIND 13 20 ATP (
SEQUENCE 245 AA; 26864 MW; OCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pobli T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO R.FASCIANS HYPOTHETICAL 21.1 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Paker's yeast).
Bukaryota: Fungi: Ascomycota: Saccharomycotins: Saccharomycets.
Saccharomycetales: Saccharomycetaceae. Saccharomyces.
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1\_HUMAN Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
20-AUG-2001 (Rel. 40, Last anno
EUKARYOTIC TRANSLATION INTILAT IF31\_HUMAN 075822; NCBI\_TaxID-9606; EIF3S1 EIF3 P35). TRANSLATION INITIATION STANDARD; Last sequence update)
Last annotation update Craniata; Vertebrata; Catarrhini; Hominidae; tion update)
FACTOR 3 SUBUNIT 1 (EIF-3 ALPHA) B Euteleostomi;

SEQUENCE

. W. B

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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE-99041954; PubMed-9822659; Block K.L., Vornlocher H.-P., Hershey J. "Characterization of conva encoding the translation initiation factor ergs."; J. Biol. Chem. 273:31901-31908(1998). p44 and

FUNCTION: BINDS TO THE 40S RIBOSOME METHIONYL-TRNAI AND MRNA.
SUBUNIT: EIF-3 IS COMPOSED OF AT LEA AND PROMOTES THE BINDING

<del>:</del> AT LEAST 10 DIFFERENT SUBUNITS

RSULTATE OF COMMENT OF entities requires a license agreement (See or send an email to license@isb-sib.ch). the This between SMISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation.

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MIM; EMBL; U97670; AAC78729.1; 603910;

Initiation factor; Protein biosynthesis

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RESULT 22
EUTJ_ECOLI
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                                                                                                                        use by non-rectification institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Hoinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                     "Construction of a contiguous 874-kb sequence of the Escherichia coli-

- K12 genome corresponding to 50,0-68.8 min on the linkage map and

analysis of its sequence features.";

DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregor J., Davis N.W., Kirkpatrick H.A., mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
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ETHANOLAMINE UTILIZATION PR
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EMBL; D90874; BAA16332.1; -.
ECOGENE; EG14184; eutJ.
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RESULT 24
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15-JUL-1998 (Rel. 36, I
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HOMEOBOX PROTEIN OTX3 (
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P41794;
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_SALTY
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"The 17-gene otherolamine (eut) operon of Sahamoella typhimurlum
encodes five homologius of carboxysome shell proteins.";

J. Bacteriol. 181:3317-3329 (1999);

1- PATHNAY: STRIANCLANTED UTILIZATION.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Actinopterygii; Neopterygii; Teleostei; Eute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence, protein expression, and mutational cohe eutE eutJ eutG eutH gene cluster."; J. Bacteriol. 177:1357-1366(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLIME-95173114; PubMed-7868611;
Stojiljkovic I., Besumler A.J., Heffron F.;
"Ethanolamine utilization in Salmonella typhimurium: nucleotide
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STRAIN-ATCC 14028S;
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SOC SEPTIFICE

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Cypriniformes; (NCBI\_TaxID-7955;

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Rasborinae; Danio.

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30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last anotation update)
20-MG-2001 (Rel. 40, Last anotation update)
PYROPHOSEHORYL-UNDECAPERDL WAGETYLGLICOSAMINE TRANSFERASE
PYROPHOSEHORYL-UNDECAPERDL WAGETYLGLICOSAMINE TRANSFERASE
[EC 2.4.1...] (UNDECAPERNYL-PP-MURNAC-PENTAPEPTIDE-UDPGLICNAC GLCNAC
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HSSS: P06601; LFJL.
ZFIN: ZDB-GENE-980526-27; otx3.
InterPro: IPR001356; Homeobox.
InterPro; IPR001356; Otx_TF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEARSCLIPES during zebrafish embryogenesis."

Brain Res. Mol. Brain Res. 27:221-231(1994)

1- FUNCTION: MAY PLAY A ROLE IN VERY ENAUX EMPROGENSIS.

1- SUNCTION: MAY PLAY A ROLE IN VERY ENAUX EMPROCESSIS.

DIENCEPHALON AND THE MIDBRAIN. MAY PLAY A ROLE IN THE ORGANIZER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00024; HOMEOBOX.
PRINTS; PR01255; OTXHOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-95206106; PubMed-7898305;
Mori H., Miyazaki Y., Morita T., Nitta H., Mish:
"Different spatio-temporal expressions of three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLILIAR LOCATION: NUCLEAR (PROBABLE).

DEVELOMENTAL STAGE: DETECTED ALONG THE MARGINAL ZONE OF SYMMETRIC DEVELOMENTAL STAGE: DETECTED ALONG THE MARGINAL ZONE OF SYMMETRIC EMBRYOS AT 5 HSS OF DEVELOPMENT AND FOUND AT THE SHELD, A PRIMARY MOREHOLOGICAL ASYMMETRY AT 6 HSS OF DEVELOPMENT, FOUND IN TWO STALFES AT THE POSTERIOR SIDE OF THE EXE RUDINENTS AT 12 HSS OF DEVELOPMENT, DISTRIBUTED IN THE DIENCEPHALON, MIDBRAIN AND THE EPIPHYSIS AT 18 HSS OF DEVELOPMENT, AND FOUND IN THE DIENCEPHALON AND THE MIDBRAIN AT 24 HSS OF DEVELOPMENT, BELORGE TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
SUBCELLULAR LOCATION:
DEVELOPMENTAL STAGE: [
                                                                                                                                                                                                                                                STRCU
                                                                                                                                                                                                                                                                                                                                                                                      GGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Developmental
38 97 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                  208
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95
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                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 I
36145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30;
Pred. No.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLN.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-SER
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACFA6C2A43A69014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mishina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otx homeoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYMMETRIC
A PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT

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"Characterization of dow cluster from Streptomycets";
Submitted (NOV-1998) to the BEBLY/GenBenk/DB2 databases.

I FUNCTION: CELL WALL ECHANTON CARALYZES THE TRANSFER OF A GICANC
SUBBHIT ON UNDECARERNIT-PROBEOSEPHORY, MERNAC-PROBEOSEPHORY, MERNACONTORY, MER
                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entities requires a license egreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        This SMISS-PROT entry is copyright. It is produced through
between the Swiss Institute of Bioinformatics and the up
the Buropean Bioinformatics Institute. There are no rest
                                                Membrane;
                                                                           Transferase; Glycosyltransferase; Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mikulik K., Zhulanova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 40733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-42684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces collinus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                      AF110367; AAD26629.1; -.
Peptidoglycan synthesis
362 AA; 38847 MW; OB
     0BBA131F2E5D5122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                        as its content is in
                                                                                                                                                                                                                                                                  Usage by
     CRC64;
                                                                                                                                                                                                                                                                             and for
                                                                                                                                                                                                                                                                                                                                                                                              EMBL
                                                                                                                                                                                                                                                                                                                                                                                         a collaboration - MBL outstation -
                                                                                                                                                                                                                                                                       commercia
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MURG_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                  Kuennen R.
Submitted
                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last anoctation update)
UDP-N-ACETYLIJUCOSAMIRE-N-ACETYLIJUCOSAMIRE TRANSFERASE
PYROPHOS PHORY—UNDECA-PRENDI N-ACETYLIJUCOSAMIRE TRANSFERASE
(EC 2.4.1...) (UNDECA-PRENYL-PP-MURNAC-PENTA-PEPTIDE-UDPGLCNAC
                                                                                             STRAIN-A3(2);
Kuennen R.A.,
   Submitted
               Rajandream M.A.;
                            Saunders D.C.,
                                          STRAIN-A3(2);
                                                       SEQUENCE FROM
                                                                                                                                                                            Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                     Q9ZBA5;
                                                                                                                                                                                                                                                                                                                                 MURG
                                                                                                                                                 NCBI_TaxID-1902;
                                                                                                                                                                Actinomycetales: Streptomycineae;
                                                                                                                                                                                                        MURG OR SC4A10.17C
                                                                                                                            EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGTSG
                                                                                                                                                                                                                                                                                                                                   STRCO
                                                                                                                                                                                                                                                                                                                                                                                                    GGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                          FROM
 (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                  (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                       N.A.
                                                                                Stadelmaier B.
N-1999) to the
                            Harris
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                          D., James
                                                                                                                                                                            Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB: Pred. No. 2.3e
1; Mismatches
                                                                              .T., McCormick J.R.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                 PRT;
                        K.D.,
                                                                                                                                                            ria; Actinobacteridae;
Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                 364
                          Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                               ₹
databases
                        J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 362;
                          Barrell B
                                                                                                                                                            Streptomyces
                                                                                                                                                                                                                                 GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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SUBUNIT ON UNDECARRENTLY ROPHOSPHORYL-MIRACC PHRAPERER OF A GICANG THREEMEDIATE I) TO FORM UNDECAPRENTL-PYROPHOSPHOSPHORYL-MIRACC (PENTAPEPTIDE)GLORNG (LIFID INTERNEDIATE II) (BY SIMILARITY). APHHAX: LAST STEP OF DEPATRO

BIOSYNTHESIS

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B
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 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SMISS-PROT entry is copyright. It is produced through a collaboration between the SMIS institute of Bioinformatics and the EMBL outstation. The EMPL outstation is the EMPL outstation in the EMPL outstation in the EMPL outstation is a long as it scontent is in no way enablished and this statement is not removed. Usage by and for commercial enables requires a license agreement (See http://www.isb-sb.ch/announce/or send an email to license@isb-sb.ch).
                                Nuclear
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
          DOMAIN
                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       Oncogene 14:745-750(1997).
                                                                                                                                                                                                                                                                                                   Sakai M., Imaki J., Yoshida K., C
Kuboki Y., Nishizawa M., Nishi S.
                                                                                                                                                                                                                                                                                                                    STRAIN=WISTAR;
MEDLINE=97190228; PubMed=9038383;
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane; Peptidoglycan synthesis SEQUENCE 364 AA; 38842 MW; D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                                                                                       EMBL; U56242; AAB50063.1; -. HSSP; P05412; 1JUN.
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                              spinal cord.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
DNA_BIND
                       DOMAIN
                                                                                      Proto-oncogene; Transcription
                                                                                                   SMART; SM00338; BRLZ;
                                                                                                             Interpro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                        *Rat maf related genes: specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GGGTAG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U10879; AAD10537.1; -
AL109663; CAB51993.1;
r protein.
139
169
180
191
212
225
ND 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
 146
173
187
194
220
234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; [
Pred. No. 2.
POLY-GLY.
POLY-GLY.
BASIC MOTIF.
                                POLY-ALA.
POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                              Cranlata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                      regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D600C5F94E9202E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                             Ogata A., Matsushima-Hibaya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3e+02;
                                                                                        DNA-binding; Activator;
                                                                                                                                                                                                                                                                                         Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 364;
                                                                                                                                                                                                                                                                                         chondrocytes, lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MAF2_MC
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Best Local Similarity
The hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQ
                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAF2_MOUSE
P54843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                        DOMAIN
                                            DNA_BIND
DOMAIN
SEQUENCE
                                                                                                   DOMAIN
                                                                                                                                                DOMAIN
                                                                                                                                                                     SMART; SM00338; BRLZ; 1.
Proto-oncogene; Transcription
                                                                                                                                                                                           MGD; MGI:96909; Maf. InterPro; IPR001871; bZIP.
                                                                                                                                                                                                               TRANSFAC; T01432; -.
                                                                                                                                                                                                                          EMBL; S74567; AAB32820.1;
HSSP; P05412; 1JUN.
                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           expression.";
Mol. Cell. Biol. 15:246-254(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurschner C., Morgan J.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C; TISSUE-Cerebellum;
MEDLINE-95097997; PubMed-7799931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                              DOMAIN
                                                                                         DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                         Nuclear protein
                                                                                                                                                                    Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 GGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                          MAF-RESPONSIVE ELEMENT BINDING. SUBUNIT: HOMO- OR HETERODIMER. SUBCELLULAR LOCATION: NUCLEAR.
   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                         139
169
180
191
207
212
225
285
313
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                                                       146
173
187
194
210
220
235
235
334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38457 MW;
                                              38655
    83
83
   39
                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30;
Pred. No.
    Score
Pred.
                                                                                        POLY-HIS.
POLY-HIS.
POLY-SER.
POLY-GLY.
                                                                    BASIC MOTIF
                                                                                POLY-GLY
                                                                                                                                                POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370
    2.3e+02;
             DB 1;
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Length 370

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a promoter that directs Purkinje neuron-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The maf proto-oncogene stimulates transcription from multiple sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PURCTION: THE C-MAP INTERACTION SITE WAS MAPPED TO THE SCOURMERS
5'-(GT)G|GC|NICT)AUTREAN 3' IN HEE L7 PROMOTER. IT MAY INTERACT
WITH ADDITIONAL BASIC-ZIPPER PROTEINS THAT DETERMINE A SUBTYPE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
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288E464708DA6C7D CRC64;
LEUCINE-ZIPPER.
76A9517EFF9C777C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                         regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                        InterPro; IPRO00598; Alabh_PNT.
InterPro; IPRO00205; NAD_binding.
Pfam: PF01262; Alabh_PNT; 1.
PROSITE: PS00836; ALADH_PNT_1; 1.
PROSITE: PS00837; ALADH_PNT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Buoinformatics and the BB the BB through Bhoinformatics Institute. There are no restruct the Buropean Bhoinformatics Institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHA_BACST STANDARD; PRT; 372 AA P17557; PRT; 190 (Rel. 15, Created) Ol-AUG-1990 (Rel. 15, Last sequence update) Ol-CUT-1940 (Rel. 30, Last annotation update ALANINE DENTIDEOGRASE (EC 1.4.1.1)
                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M33299; AAA22211.1; -. PIR; B34261; B34261.
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STRAIN-IFO 12550;
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Geobacillus.
         175
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MISCELLANBOUS: THE B.STEAROTHERMOPHILUS ENZYME RETAINED ABOUT 50
OF ITS INVIAL ACTIVITY WHEN HEAVED AT 85 DEGREES CELSIUS FOR 5
MIN AT PH 7.2, WHEREAS THE B.SPHAERICUS ENZYME LOST THE SAME
ACTIVITY WHEN HEAVED AT ONLY 65 DEGREES CHESIUS FOR 5 MIN.
SIMILARITY: STRONG, TO OTHER ALANINE DEHYDROGENASES AND PARTIAL
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GGGTAG 180
                                                 GGGTSG 6
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                                                                                                Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
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372 A
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                                                                                                                 . 38
                                                                                                                    Score 30; [
Pred. No. 2.
                                                                                                                                                                                                           POTENTIAL.
NAD (BY SIMILARITY).
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RESULT 30
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                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1
SMART; SM00132; LIM; 2
PROSITE; PS00478; LIM_DOWAIN_1; 2
PROSITE; PS50023; LIM_DOWAIN_2; 2
PROSITE; PS50027; HOMEDBOX_1; 1
PROSITE; PS50071; HOMEDBOX_2; 1.
                                        DOMAIN
                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  German M.S., Wang J. "Chadwick R.B., Rutter H.J.;

"Synergistic activation of the insulin gene by a LIM-homeo domai protein and a basic healty cop-halty protein: building a functio insulin minisoriancer complex".

Insulin minisoriancer complex T. The Complex T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1. Pfam; PF00412; LIM; 2. ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC: T01958; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
          SEQUENCE
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                                                                                                                     NIAMOC
                                                                                                                                                                                       Franscription
                                                                                                                                                                                                                                LIM domain;
                                                                                                                                                                                                                                                              Homeobox; DNA-binding;
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                                   on regulation.
35 85
94 147
195 254
257 265
                                                                                                                                                                                                                      Repeat; Metal-binding; Zinc;
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(Rel. 29, Last seq
(Rel. 39, Last ann
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                                                                                                                                                                                                                                                         Developmental protein;
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                                                                                                                LIM 1.
LIM 2.
POLY-GLN.
2675E6F298EE9486 CRC64;
                                                                            HOMEOBOX
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SERCLYEAST

TO SERCLYEAST

AC P33330

AC P3330

AC P3330

AC P3330

TO 1-FREE

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DT 15-DREE

DR SECOLE

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Query Match
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"A gene from Saccharomyces cerevisiae which codes for a
significant homology to the bacterial 3-phosphoserine
annotransferase."
Yeast 10:385-388(1994)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last sendent update)
PHOSPHOSERIME ANINOTRANSFERASE (EC 2.6.1.52) (PSAT).
SEIL OR SEIC OR YORLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERC_YEAST
P33330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L20917; AAA20886.1; -. EMBL; U19714; AAA85703.1; -. EMBL; Z75092; CAA99393.1; -. EMBL; Z42680; S42680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SRISS-PROT entry is copyright. It is produced through a collaboration between the Skiss Institute of Butoinformatics and the EMBL outstation - the Buropean Bioinformatics institute are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license/sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
-1- CATALYTIC ACTIVITY: O-PHOSPHO-L-SERINE + 2
3-PHOSPHONOOXYPYRUVATE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-94287715; PubMed-8017107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                             Pfam; PF00266; aminotran_5; 1.
ProDom; PD001544; Phosphser_amintransf; 1.
PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - 1 - COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                       SEQUENCE
                                                                                                                                                             CONFLICT
                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                           Serine biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-2DPAGE; P33330; YEAST
                                                                                                                                                                                       Pyridoxal phosphate.
BINDING 218 2
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000192; Aminotransf_class_V.
InterPro; IPR003248; Phosphser_amintransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: REQUIRED BOTH IN MAJOR PHOSPHORYLATED PATHWAY BIOSYNTHESIS AND IN THE BIOSYNTHESIS OF PYRIDOXINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                     S0005710; SER1.
   Similarity
5; Conserv
                                                                                                                                    258
395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuenzler M.,
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetaceae; Saccharomyces
                                                                                                                                       259
43415
                             90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/Ge
                                                                                                                                       MW;
   Score 30; DB
Pred. No. 2.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                       FD -> LH (IN REF. 2
; A22F020CC969B4BC
                                                                                                                                                                 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FD -> LH (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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1.5e+02;
0;
                                                          DB 1;
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2 OXOGLUTARATE
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                                                       Length 395
                                                                                                                                       CRC64;
       Indels
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DDL_TREPA

STANDARD: PRT: 396 AA.

DDL_TREPA

STANDARD: Last sequence update)

DDL_TREPA

DDL_TREPA

STANDALD: ALA LIGASE; LIGASE (EC 6.3.2.4) (D-ALANKIALANKINE SYNTHETASE)

DDL_TREPA

DDL
MURG_MYCLE
ID MURG_MYCLE
AC 069552;
DT 30-MAY-2000
DT 30-MAY-2000
                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                              1 GGGTSG
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                                                                                                                                                                                                                        GGGTAG
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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(Rel.
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                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                   STANDARD;
   39,
                                                                                                                                                                                                                                                                                                                                                          90.9%;
                          Created)
                                                                                                                                                                                                                                                                                                                               Pred. No. 2.5e+02;
1; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                        Score 30;
                                                                                       PRT;
                                                                                       407
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                    Length 396;
                                                                                                                                                                                                                                                                                                                                   Indels
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d.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local s
Matches 5
                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Greated)
30-MAY-2000 (Rel. 39, Last sequence update)
30-AMG-2001 (Rel. 30, Last sequence update)
UDP-N-ACETYLGUCOSANIES-N-ACETYLGULGOSANIES TRANSFERSE
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGULGOSANIES TRANSFERSE
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGULGOSANIES TRANSFERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURG_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Glycosyltransferase; Cell division; Peptidoglycan synthesis; Complete proteome. SEQUENCE 407 AA; 42422 MW; B757B73C092C53F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL022602; CAA18668.1; -. EMBL; AL583920; CAC31295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLGUICOSAMINE-TRANSFE
PYROPHOSPHORYL-UNDECAPRENQL N-ACETYLGLUCOSAMINE TRANSFE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leproma; ML0914; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21128732; PubMed-11234002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
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                                                                                                                                                                                    2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTAG
                                                                                                               RV2153C OR MT2212 OR MTCY270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
     Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB
Pred. No. 2.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacillus
Mycobacteriaceae;
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64
Mycobacterium
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                                                                                                                                                                                    GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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(LIPID
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RESULT 35

YASB_MCTU

ID YASB_MTCTU STANDARD; PRT; 453

AC 053416;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence upda
DT 20-AMG-2001 (Rel. 40, Last annotation up
DE HYPOTHETICAL PE-PERS FAMILY PROTEIN RV10
GN RV1058C OR MY1097 OR MY017 21C.
OS MYCobacterium tuberculosis.
OC Accinomycecales; Corynobacterineae; Myco
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A WEDILINE-99235987; PubMed-9634230;

A Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III. Tekela F.,

A Gordon S.V., Eiglaneier K., Gas S., Barly C.E. III. Tekela F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Bayles R., Devlin K., Feltvell T., Gentles S., Hamlin N., Holroyd S.,

A Horisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Cliver S., Osborne J., Ouall M.A., Rajndream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.E., Taylor K., Miltehead S., Barrell B.G.,

Toelphering the biology of Mycobacterium tuberculosis from the

RIT complete genome sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Glycosyltransferase; Cell division; Cell wall; Paptidoglycan synthesis; Complete proteome. SPUDENCE 410 AA; 41860 MW; 9990ZAFE35FE73DB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Feterson J. DeBoy R., Dodson R., Culman M.D., Helboy E.,
Kolonay J.F., Nelson M.C., Umayon L.A., Ernolaeva M.D., Salzberg J.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Nikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TubercuList, Rv2153c; -
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SUBCELLULAR LOCATION: MEDIRARIE ASSOCIATED (BY SIMILARITY).
SINILLARITY: BELONGS TO THE WING FAMILY.
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Mycobacteriaceae; Mycobacterium

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P52707;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
(R)-MANDELONITRILE LYASE 150FORM 3 PRECURSOR (BC HYDROXYWITRILE LYASE 3) (R)-OXYMITRILASE 3).
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                                                                                                            PRUSE
                                                                                                                                                                                                                                                                                                                                              Hypothetical protein;
CONFLICT 218 211
CONFLICT 235 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL021897; CAA17184.1; .. EMBL; AE006991; AAK45353.1; ALT_INIT TIGR; MT1097; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bh the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed Usage by ancentified and this statement is not removed Usage by ancentified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison laboratory strains."; Submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonsy J.F., Melson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-CDC 1551 / Oshkosh Fleischmann R.D., Alland
                                                                                                                                                                                                                                                                                                         SEQUENCE
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tical protein; Complete
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Plant Physiol, 115-1159-1369(1997).

Plant Physiol, 115-1159-1369(1997).

PLANTION: TRYOLVED IN CYANOGENIS, THE RELEASE OF HEN FROM INJURED THE SUBES. CATALYSES THE STEEDGEPECIFIC ADDITION OF HEN TO A VARIETY OF ALDERTHES IN UTITO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NUTROGEN.

1- COPACTOR: FAD.

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SIGNAL 1
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PROSITE; PS00624; GMC_OXRED_2; 1
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EMBL; AF013161; AAB67714.1; -.
InterPro; IPR000172; GMC_oxred
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Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; undicotyledons;
eurosids I; Rosales; Rosaceae; Prunus.
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SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY
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SUBUNIT: MONOMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Rosidae;
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Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR000172; GMC_oxred.
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CATALYTIC ACTIVITY: MANDELONITRILE - CYANIDE + BENZALDEHYDE
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SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY
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37. Last annotation update)
E LYASE ISOFORM 2 PRECURSOR (EC 4.1.2.10)
YASE 2) ((R)-OXYNITRILASE 2).
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PAD (ADP PART) (PROBABLE).

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Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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**Prediction of the coding sequences of 100 new CDMA clones from brain which code to 100 new CDMA clones from brain which code to 100 new CDMA clones from the CDMA clones from the CDMA clones from the CDMA clones for all throughout the consists of at 100 new CDMA clones from the ECCEPTOR COMPLEX THAT CONSISTS OF AT 1.5 SUBJECT THE TREET BROWNING THE CONSISTS OF AT 1.5 SUBJECT THE TREET FOR THE CONSISTS OF AT 1.5 SUBJECT THE CONSISTS OF AT 1.5 SUBJE
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last anotation update)
MITOCHOMDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (TRANSLOCASE OF OUTER
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Tanaka A., Kotani H., Nomura N., Ohara
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European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY: CONTAINS 10 TPR REPEATS.
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BA KAGANUM J. Shinogawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Raka K., Kasawa K., Taoda M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I., Ba Kagawa K., Zaoda M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I., Raka Kagalto T., Okazaki Y., Gojbobri T., Bond H., Kasakawa T., Saito R., Rakadota K., Matudda H.A., Ashburner M., Betalor S., Cozavant T., Rakadota K., Matudda H.A., Ashburner M., Betalor S., Cozavant T., Rakadota K., Matudda H.A., Ashburner M., Betalor S., Cozavant T., Rakadota K., Matudda H., Ashburner M., Betalor S., Cozavant T., Rakadota K., Magner L., Washio T., Rakadota K., Magner L., Washio T., Rakadota K., Betalor S., Magner L., Washio T., Rakadota K., Washio T., Rakadota K., Washio T., Mashio T., Magner L., Washio T., Washio 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AUTOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (TRANSLOCASE OF OUTER
                                                        REPEAT
                                                                                           REPEAT
REPEAT
                                                                                                                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                 EMBL; AK012084; BAB28018.1; .. MGD; MGI:106295; D16Wsu109e.
                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/mnnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
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                                        REPEAT
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TPR 3.
TPR 4.
TPR 4.
TPR 6.
TPR 6.
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TPR 7.
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NP_BIND
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SEQUENCE
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TIGR; TM0480; -.
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the European Bioinformatics Institute. There are no rest
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Pfam; PF00005; ABC_tran;
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                                   1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: CONSISTS OF THREE SUBUNITS: UVAA, UVBB AND UVRC.
SUBCELUULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENTINE HEAD RECORD NUCLEATION OF THE ABCHION OF UV-DAMAGED NUCLEATION SEGMEN PRODUCING OLIOOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN AND A DNA-BINNING PROFEIN THAT PREFERENTALLY BINDS SINGLE-STRANDED ON UV-TRRALIAFIED DOUBLE-STRANDED DNA [8] SIMILARITY).
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Zinc-finger: Complete proteome.
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17 624 ATP (POTENTIAL).
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Q9tm74 rhynchosteg Q9tm63 platyhypnid Q9tm63 platyhypnid Q9bzi7 homo sapien Q9vse9 drosophila Q9a4m2 caulobacter Q9aa21 caulobacter

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Ol MAR-2001 (TERMILTEL 15. Last sequence update)
Ol MAR-2001 (TERMILTEL 15. Last annotation updat
GROWNIC DAM, CHROMOSOME 5. TMC CLONE:K22720.
Architopsis thailains (Wouse-ear cress)
                                STRAINE-MAASTRICHT:
MEDLINE-96357047: PubMed-8764031:
VInk.C. Beaken E., Bruggeman C.A.:
"Structure of the at cytomegalovirus
J. Virol. 70:522-5229(1956):
                                                                                                                                 PR171.1.
R171.1.
STRAIN-MAASTRICHT;
MEDLINE-20366325;
                                                                                                      Rat cytomegalovirus (strain Maastricht).
Viruses; dsDNA viruses, no RNA stage; He
Betaherpesvirinae; Muromegalovirus.
                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopais thaliana or Sequence features of the regions of 1.013,767 physically assigned P1 and TAC clones."; DNA Res. 5:297-308(1998).
EMBL, ABO16973; BAB10357.1; -
SEQUENCE 218 AA; 22937 MN; C8551D884AB1FFG
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Spermatophyta; Magnollophyta; eudiocryladons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                  SEQUENCE FROM
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09k3H9 caulobacter
09k3H8 drosophila
09k01 phocoena sp
067206 aquifex aeo
09rp97 burkholderi
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Gruilthuijsen Y K. Beuken E. Bruggeman C.A.,
"Rat Cyromegalovius R89 is a highly conserved
spliced transcript".
Vitus Res. 69.119-130(2000)
Witus Res. 69.119-130(2000)
BMIL: AF337689; AF992681;
EDUIDENCE 221 Ax; 24489 MM; CD36BC51A9AB69B3
                                                                Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHOTRANSFERASE LACE (FRAGMENT).
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pfam; PF00457; Glyco_hydro_11; 1.
priNTS; PR00911; GLHYDRLASE11.
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"Transformation of Piromyces communis xylanase to
Submitted (NGC-2000) to the EMBL/GenBank/DDbJ data
EMBL; AF297649; AAG18439.1;
                                                                                                                                                                                                                                                                                                                                                               Piromyces communis.
Eukaryota; Fungi; Chytridiomycota;
Neocallimasticaceae; Piromyces.
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                 NCBI_TaxID-1302;
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Bacteria; Firmicutes; I
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DNA sequence of the rat cy
74:7656-7665(2000).
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01-UNY-2001 (TERRILE). 17 Last annotation update)
LUNX PROFEIN (NASOPHARYNGEAL CARCINOMA-RELATED PROFEIN) (TRACHEAL EPITHELLUM EMELICUED PROFEIN) (BA49010.5) (LUNX PROFEIN (LOCS.1297)).
LUNX OR PLUNC OR BA49010.5.
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                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                         TISSUE-LUNG;
                                                                                                         SEQUENCE FROM
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Submitted (DEC-1999) to the EMBL; AF210773; AAG39000.1;
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InterPro, IPR003501; PTS_IIB.
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RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A. Adalle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashbarner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashbarner M., Henderson S.N.,
RA Sutton G.G., Wortuna J.R., Yandell M.D., Zhang M., Henderson S.N.,
RA Sutton G.G., Wortuna J.R., Yandell M.D., Zhang M., Heidfer B.D.,
RA Harli D., Robers Y. H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Harli J.F., Aghbayani A., An H.J., Handres P.F., Malson C.N., Malson C.N., Malson C.N., Malson C.N., Bashards D., Borthon D., Borthon M.B., Bound J., Barnate D., Borthon C.S.,
RA Harli J.F., Manna A., Barnate D., Barnate D., Borthon C.S.,
RA Harli J.F., Bance P.V., Benne P.P., Banderi D., Bothice P., Martis R.,
RA Heeson K.Y., Benne P.V., Bernate D., Bothice R., Center A., Chandra I.,
RA Heeson K.Y., Benne P.V., Benne P.P., Banderi D., Bothice P.,
RA Hortis K.G., Lowley S., Dahike C., Joyden R.C., Mayor B.C., Duin P.,
RA Ge Pablos B., Delber A., Dahne G., Mayor M.S., Dalvis B.C., Duin P.,
RA Gerbin D., Bernate B., Conferra G., Ferritara S., Fleischmann W.,
RA Hootson K.J., Bernate B.C., Gerber H.M., Glasser K.,
RA Hootson K.J., Bernate B., Conferra G., Ferritara S., Fleischmann W.,
RA Hortis M.L., Harrey D., Freichmann F., Gurder B., Harris M.,
RA Holait M., Kalush F., Karpen G.H., Well M.-H., Harris M., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraff C., Kravitz S., Malp D., Lait Z.,
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MEDLINE-20472055;
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Liu W.D., Zhou W., Wang L.,
"cloning a new gene related
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 Wilson R. Ainscough R. Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Coper J., Coulson A. Bonfield J., Burton J., Connell M., Copsey T., Coper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Pulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Lattellie P., Jones M., Kershaw J., Kirsten J., Laister N., Lattellie P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Lightning J., Thomas K., Vander B., Studen R., Sultern J., Shownkeen F. Smaldon N., Smith A., Sonnhammer B., Staden R., Sultston J., Thomas K., Vandin M., Vaughan K., Waterston R., Hatton A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                              SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                               Submitted
                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryots; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NeBI_TaxID=6239;
                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01228; EGGSHELL.
PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FB90030408; CG11085.
InterPro; IPR002952; Eggshell.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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- SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
EMBL, AE003499 AP648182.1; -.
HSSP; P22808; 1NK3.
                                                                                                                                                            Gardner
                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                Y22F5A.5 PROTEIN.
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Similarity 100.
6; Conservative
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Pred. No.
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1.7e+02;
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RESULT
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Nature 368:32-38(1994).
EMBL: ALO21479; CAA1632
SEQUENCE 279 AA; 302
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O9LYP4;
O1-OCT-2000 (7
O1-OCT-2000 (7
O1-OCT-2001 (7
HYPOTHETICAL (7
T28J14_160
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080450;
01-NOV-1998
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ROUNDSLEY S. D., KRUL S., LIN X., Ketchum K.A.,
Brandon R.C., Sykes S.H., Mason T.H., Kerlavas
Somervillo C.R., Venter J.C.,
Arabidopsis thaliana chromosome II BAC P16H14
Arabidopsis thaliana chromosome II BAC P16H14
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
EMBL, AC003028, AAC2714 1.;
InterPro; IPR001005; Myb_DNA_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-NOV-1998 (TremBLrel.
01-JUN-2001 (TremBLrel.
PUTATIVE GTL1 PROTEIN.
Bevan M., Murphy G.,
Rudd S., Lemcke K.,
Submitted (APR-2000)
                                                                                                                                                                                  Arabidopsis thalians (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta: Magnoliophyta: eudloctyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00395; SANT; 1.
SEQUENCE 289 AA; 34307 M
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                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID-3702;
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AA; 30291 M
    Mayer K.
) to the
                             Ridley P.,
Mayer K.F.X
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Pred. No. 1.7
0; Mismatches
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                                                                    Bancroft I.,
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age A.R., A
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EMBL/GenBank/DDBJ

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RESULT
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ID 07
AC 07
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Best Local :
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Best Local :
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InterPro: IPR003130, GED.
InterPro: IPR00525; Ubiquitin.
Pfam: PF02179; BAG; 1.
SMART: SM0256; BAG; 1.
SMART: SM00302; GED; 1.
                  075953;
01:NOV-1998 (TrEMBLrel. 08,
01:NOV-1998 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
HEAT SHOCK PROTEIN HSP40-3.
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SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2001 (TREMBLREL. 17, Last annotation update)
REVERSE TRANSCRIPTASE-LIKE PROTEIN (FRAGMENT).
                                                                  075953
                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                 Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                             Bunikis J., Hall L., Barbour A.G.; "Reverse transcriptase-like sequen
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Bunikis J., Hall L.,
                                                                                                                                                                                                                                                                                                                                                                 Amblyomma americanum.
Eukaryota; Metazoa; Arthropoda; Chelicerata;
          Homo sapiens (Human)
                                                                                                                 175
                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                RNA-directed DNA polymerase
                                                                                                                                                                                                                                                     InterPro; IPR000477;
                                                                                                                                                                                                                                                                                                      americanum."
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6943;
                                                                                                                                                                                                                                                                                                                                                            Parasitiformes; Ixodida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Submitted (APR-2000) to the EM
EMBL; AL163652; CAB87278.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50053; UBIQUITIN_2;
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35459
 Chordata;
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the EMBL/GenBank/DDBJ databases
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Pred. No.
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Pred. No.
Craniata;
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                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                    core 33; DB 5;
ced. No. 1.9e+02;
Mismatches 0;
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annotation updat
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Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                           the tick Amblyomma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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                            update)
                                                                                                                                                                       Length 315;
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Q9GE43
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Best Local Similarity
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SMARF; SM00271; DnaJ_; 1.
PROSITE; PS00636; DNAJ_1; 1
PROSITE; PS50076; DNAJ_2; 1
Heat shock.
       - CAPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) -
- PHOSPHO-D GIATCHARTE + 2-HOSPHOGIATOLATE.
- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
- SYMILARITY BELONGS TO THE RUBISCO LARGE CHAIN FAHILY.
EMBLY, AC233567; AAC27527.1;
- INTERPRO: IPRO00685; RUBISCO_LATGE.
- PROSTRE: PRODICTS; RUBISCO_LATGE.
- PROSTRE: PRODICTS; RUBISCO_LATGE.
- PROSTRE: PRODICTS; RUBISCO_LATGE.
- CGIDDON disvide fixation; Chloroplast; Lyase, Monooxygenase;
                                                                                                                                                                                                 DE Luna E., Buck W.R., Aklyama H., Arikawa T., Tsubota H.,
Gonzalez D., Newton A.E., Shaw A.J., Gonzalez D.;
"Ordinal Bhjogeny within the Bypobryalean Pleurocarpous
Inferred from Cladistic Analyses of Three Chloroplast DNA
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridipl
Bryopsida; Bryidae;
NCBI_TaxID=94508;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TERMILTE1. 16, Late sequence update)
01-MAR-2001 (TERMILTE1. 16, Late sequence update)
01-UN-2001 (TERMILTE1. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT) (FRAGMENT).
Oxidoreductase; Photorespiration; Photosynthesis
                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudoscleropodium purum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GE43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Differential response of members in the hsp40 family to stress agents in mammalian colls.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen M.S., Laszlo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002939;
InterPro; IPR001623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGTSG
                                                                                                                                             REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SACTIVE SITE (BY SIMILARITY).

CAPALITIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) - PHOSPHO-D-GLYCERATE.
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                                                                                                                                                                                                                                                                                                                                                                          Streptophyta; Embryophyta; Bryophyta;
les; Brachytheciaceae; Pseudoscleropodium.
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Pred. No.
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Best Local
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Best Local
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NON_TER
SEQUENCE
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   003112
                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Phylogeny of Salaginellaceae: evaluation of generic/subgeneric relationships based on rold gene sequences.", Int. J. Plant Sci. 160:585-594(1999)

1 FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF INBULSE: 1,5-BISHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRANCHIATION THE PENTORS SUBSTRATE IN THE PHOTORESFIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTAREOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMULTAREOUSLY AND IN COMPETITION TO THE SAME ACTIVE SITE (BY SIMULTAREOUSLY AND IN COMPETITION OF COMPANY.)

- CAPALTTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopodiophyta;
Selaginella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TERMBLrel. 13, Created)
01-MAY-2000 (TERMBLrel. 13, Last sequence update)
01-MIN-2010 (TERMBLREl. 17, Last sequence update)
01-UN-2011 (TERMBLREL 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00157; RUBISCO_LARGE; 1. Carbon dioxide fixation; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000685; RuBisCO_large. Pfam; PF00016; RuBisCO_large; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selaginella denticulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARGE SUBUNIT) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00880; 1RBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=50508;
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6; Conser
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illarity 100.
Conservative
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   PRELIMINARY;
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427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptophyta; Embryophyta; Tracheophyta; 
da; Selaginellales; Selaginellaceae;
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Pred. No. 2.8
D; Mismatches
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Pred.
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   PRT;
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   449
                                                                                                                                                                                                                                                                                                                                                                                                Lyase; Monooxygenase;
                                                                                                                                                                                           DB 8;
2.8e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LARGE CHAIN FAMILY
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Best Local S
Matches
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 17, Last acquence update)
01-JUK-2001 (TrEMBLrel. 17, Last annotation update)
11-JUK-2001 (TrEMBLREL. 17, LAST annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASS LARGE CHAIN (EC 4
                                                                                                                                                                    Q31681 PRELIMINARY; PRT; 451 AA.
Q31681,
Q11681,
Q1.NOV-1996 (TREMBLrel. Q1, Created)
Q1.NOV-1996 (TREMBLRel. Q1, Last sequence update)
Q1.NOV-1996 (TREMBLRel. 17, Last sequence update)
Q1.JUN-2001 (TREMBLRel. 17, Last s
                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
NON_TER
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Mendel; 23015; Lophe:rbcL; 23015.
InterPro; IPR000689; RUBISCO_Large; 1.
Pfam; PF00015; RUBISCO_LARGE; 1.
PROSTTE; PS00157; RUBISCO_LARGE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jungermanniales;
NCBI_TaxID=3207;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Mol. Phylogenet. Evol. 0:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Jungermanniales; Geocalycinae; Lophocoleaceae; Lophocolea.
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"Phylogenetic analysis 
Mol. Phylogenet. Evol.
                                     SEQUENCE FROM N.A. MEDLINE=94356259;
                                                                           NCBI_TaxID=13797;
                                                                                        Andreaeopsida;
                                                                                                                   Chloroplast
                                                                                                                                              RBCL
                                                                                                                                                         LARGE SUBUNIT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase;
                           Manhart J.R.;
                                                                                                      Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                Andreaea rupestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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                                                                                                                                                                                                                                                                                                    392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHO-D-GLYCERATE.

PHOSPHO-D-GLYCERATE + O(2) = CANALYTIC ACTYVTY: D-RIBBLOSE 1,5-BISPHOSPHATE + O(2) = PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

BHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

SUBCULT: 0 LARGE CHAINS + SWALL CHAINS.

SUBCULTAN LOCATION: CHLOROPLAST.

SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                             1 GGGTSG
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SIMILARITY: BELONGS TO THE
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CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2
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                                                                                                                                                                                                                                                                                                    GGGTSG
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Llarity 100.0%;
Conservative (
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                                                                                                                                                         (FRAGMENT).
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                                                                                            Andreaeales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Photorespiration;
                                         PubMed-8075831;
                                                                                                                                                                                                                                                                                                                                                                                                                                    449
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191
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 of green plant rbcL
3:114-127(1994).
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                                                                                            Andreaeaceae;
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Pred. No.
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                                                                                                      Embryophyta;
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s 0;
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              sequences.";
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ACTIVATES
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Matches
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PROSITE; PS00157; RUBISCO_LARGE: 1.
Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
Oxidoreductase; Photorespiration; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TERMELFel. 17, Created)
01-JUN-2001 (TERMELFel. 17, Last sequence update)
01-JUN-2001 (TERMELFel. 17, Last anotation update)
01-JUN-2001 (TERMELFel. 17, Last anotation update)
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                         Q9ВСК9
                                                              SEQUENCE
                                                                             Chloroplast.
                                                                                             "Molecular phylogeny of brown algal genera Akkesiphycus and (Laminariales), resulting in the circumscription of the new Akkesiphycaceae and Halosiphonaceae."; Phycologia 39:415-428(2000).
                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SETO INLAND SEAS.
KAWAI H., SASAKI H.;
                                                                                                                                                                  Desmarestiaceae; I
NCBI_TaxID-114257;
                                                                                                                                                                                   Eukaryota; stramenopiles; Phaeophyceae; Desmarestiales;
                                                                                                                                                                                            Chloroplast
                                                                                                                                                                                                      Desmarestia
                                                                                                                                                                                                                                                                 Q9BCK9;
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                                                                      NON_TER
                                                                                                                                                                                                                       (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                       Match
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CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHAYE, THE PRIMARY EVENT IN PROTOSYMPHETIC CARBON DIOXIDE EIXATION, AS WELL AS THE OXIDATIVE FRACHAUNTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
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  GGGTSG
                                                                                      AB037141; BAB32897.1; -.
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6; Conser
                          Similarity
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ilarity 100.0%;
Conservative
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llarity 100.0%;
Conservative (
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193
451
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51314 MW;
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Pred. No. 2.5
); Mismatches
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                            Pred. No.
                                   Score 33;
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                                                              61A1F7C2DFA82D45 CRC64
                   Mismatches
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No.
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                            3e+02;
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                   Indels
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                                                                                                                Halosiphon
families
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Best Local (
Matches
                                           Q9H1J0;
Q9H1J0;
01-MAR-2001
01-MAR-2001
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NON_TER
SEQUENCE
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"Phylogeny of the eudicots: a nearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9GHW8;
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                          HUPF3B
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                                                                                                                                                                                                                                                                                                                                                                                               on rbcL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gomphandra javanica
                                                                                                                                                                                                                                             Pfam; PF00016; RuBisCO_large;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=124965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARGE SUBUNIT) (FRAGMENT).
                                                                                                                396
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                                                                                                              GGGTSG 401
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6; Conserv
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(TrEMBLrel.
(TrEMBLrel.
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                                                                     PRELIMINARY;
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51914
  Primates;
         Chordata;
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16,
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Pred.
                                                                     PRT;
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- CARACYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSHATE + O(2) -
PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCCATE.
- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
EMBL; AA402954; CAC04312.1;
INTERFORM: TO THE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00016; RuBisCO_Large; 1.

PROSITE; PS00157; RUBISCO_LARGE; 1.

Carbon dioxide fixation; Chloroplast; Lyase; Mono Carbon dioxide fixation; Chloroplast; Lyase; Mono Coldoreductase; Photorespiration; Photosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicoty; dedons; core eudicots;
Asteridae; euasterids II; Icacinaceae; Gomphandra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROCESS OF SEQUENCES:
Bull 55:257-309(2000)
FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE PROTOSETRATE IN THE PROTOSE SUBSTRATE IN THE PROTOSESPICATION PROCESS. BOTH REACTIONS COCHR SIMILIARITY).
REACTIONS COCHR SIMILIARITY. AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMILARITY).
CATALYTIC ACTIVITY: D. TRIBULOSE 1.5-BISPHOSPHATE + CO(2) - 2 3-PHOSPHO-D-GLICERNIE.
                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC18693698AD95FE CRC64;
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Q9TM74
                                                                                                                                                                                                                             -1. CATALITIC ACCURATE.

PHOSPIO-D-CLYCELATE.

-1. CATALITIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHATE + O(2) = 3-
PHOSPIO-D-CLYCERATE + 2-PHOSPHOGLYCOLATE.

-1. SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

-1. SUBULITY: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

-1. SIMILARITY: BELONGS TO THE NUBISCO LARGE CHAIN FAMILY.

-1. SIMILARITY: BELONGS TO THE SUBISCO LARGE CHAIN FAMILY.

REBBL, ADDA4944 BAA6213.1;

RICHEROLOGIS, RUBISCO LARGE: 1.

RICHEROLOGIS, RUBISCO LARGE: 1.

RPAGN:TE: PS00157; RUBISCO LARGE: 1.

RPAGN:TE: PS00157; RUBISCO LARGE: 1.

RPAGN:TE: PS00157; RUBISCO LARGE: 1.

RW COTDON GLOXIDE FAMILY.

RW OXION: GLOXIDE FAMILY.

RW OXI
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A preliminary phylogeny of Hypnales (Musci) as inferred from chloroplast riot, sequence data.";

Bryol Res. 7:233-748 (1999).

1- FUNCTION: RUBISCO CATALYESS TWO REACTIONS: THE CARBOXYLATION OF D-1-FUNCTION: RUBISCO CATALYESS TWO REACTIONS: THE CARBOXYLATION OF D-1-FUNCTION CONTROL OF THE PRIMARY EVENT IN PHOTOSSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESIFICATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE TREE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE CARBOXYLATION COMPETITION AT THE CARBO
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01-MAY-2000 (TTEMBLIEL 13, Last sequence update)
01-JUN-2001 (TTEMBLIEL 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lykke-Andersen J., Shu M.-D., Steatz J.A.,
"Human Upf proteins target an mRNA for non
bound downstream of a termination codon.";
Cell 103:1121-1131(2000).
BMBL: ANO13251; ANG48511.1;
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Deguchi H., Seki T.,
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NCBI_TaxID=90343;
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Bryopsida;
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SEQUENCE FROM N.A.
PubMed=11163187;
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6; Conser
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Hlarity 100.
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Hypnales; Brachytheclaceae; Rhynchostegium
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56213 MW;
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Pred. No.
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Best Local
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Q9BZI7;
-01-JUN-2001
01-JUN-2001
01-JUN-2001
SEQUENCE FROM N.A.
MEDLINE-20565755; PubMed-11113196;
Serin G., Gersappe A., Black J.D.,
"Identification and characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9TM63;
Q9TM63;
Q1-MAY-2000
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PROSITE: P900157; RubisCo_LakeG: Lyase: Monooxygenase:
Carbon dloxide flation: Chloroplast: Lyase: Monooxygenase:
Oxidoreductase: Photorespiration: Photosynthesis.
SBQUENCE 475 AA: 52740 MH: C25F555155A15EEC CRC64;
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- CATANTYLE ATTE (BY SIMILARITY).

- CATANTYLE ACTIVETY: D-RIBULOSE 1.5-BISPHOSPHATE + CO(2) = 2:

- PHOSPHO-D-CIXVERNE, B-REBULOSE 1.5-BISPHOSPHATE + O(2) = 3:

- PHOSPHO-D-CIXVERNE + 2-PHOSPHOGIXVOLATE - O(2) = 3:

- PHOSPHO-D-CIXVERNE + 2-PHOSPHOGIXVOLATE - SIMILARITY).

- I SUBCELLAIRS LOATION: CHLOROPLATE (BY SIMILARITY).

- I SUBCELLAIRS HOAGE CHAINS - ON THE RUBISCO LARGE CHAIN FAMILY.

I BILDHIT: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.

I BILDHIS: BARGEOG 1.

- PHOSPHOTO: PHOSPHOSO STREET - ON THE PROBLESS - PHOSPHOTO: SHIPPOND STREET - ON THE PHOSPHOTO: SHIPPOND SHIPPO
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Mammalia; Eutheria;
                                                                                                                                                                                                   UPF3X.
                                                                                                                                                                                                                        UPF3X.
                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                         Homo sapiens
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Bryol. Res. 7:233-248(1999).
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Deguchi H., Seki T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TERMELTAL 1.1), Last sequence update)
01-UN-2001 (TERMELTAL 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bryopsida; Bryidae; Hypnales;
NCBI_TaxID=98942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platyhypnidium riparioides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    403 GGGTSG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                          22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RUBISCO CATALYSES TWO RIBULOSE 1,5-BISPHOSPHATE, THE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
6; Conserv
  Gersappe A., Black J.D., Ar cation and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSUBOTA
                                                                                                                                                                                                                                      (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                         (Human)
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                                                                                                                                Chordata;
Primates;
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17,
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les; Brachytheciaceae; Platyhypnidium.
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Last annotation update)
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Catarrhini;
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Pred. No.
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                       Aronoff R.,
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     of human orthologues
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i; Hominidae; Homo.
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                       Maquat L.E
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RA Ballew R., Baud A., Baxendale J., Bayraktarogu L., Beasley E.M.,
Ra Beeson K.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ra Borkova D., Botchan M.R., Bouck J. Brokstein P., Brottler P.,
Ra Burtis K.C., Busam D.A., Batler H., Cadieu E., Center A., Chandra I.,
Ra Burtis K.C., Busam D.A., Batler H., Cadieu E., Center A., Chandra I.,
Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,
Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise R.,
Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Ra Hostin D., Houston K.A., Hernandez J.R., Houck J.,
Ra Hostin D., Houston K.A., Howland T.J., Mai M.-H., IDsyamn C.,
Ra Jalaii M., Kalush F., Karpen G.H., Ke Z., Kenitson J.A., Ketchum K.A.,
Ra Hostin D., Houston K.A., Howland T.J., Mai M.-H., IDsyamn C.,
Ra Jalaii M., Kalush F., Karpen G.H., Ke Z., Kenitson J.A., Ketchum K.A.,
Ra Hostin D., Houston K.A., Howland T.J., Mai M.-H., IDsyamn C.,
Ra Jalaii M., Kalush F., Karpen G.H., Ke Z., Kenitson J.A., Ketchum K.A.,
Ra Hostin D., Houston K.A., Howland T.J., Mai J., Jai Z.,
Ra Lux M., Mattel B., McInnosh T.C., McIecd M.P., McBarcon D.L.,
Ra Mannt S.M., Noy M., McIphy L., Mazzy D.M., Nolson D.L.,
Ra Mannt S.M., Noy M., McIphy L., Mazzy D.M., Nolson D.L.,
Ra Mailiams S.M., Noodon K.A., Mixon K., Nasskern D.R., Ponleb J.M.,
Ra Palazzon D. M., Pittana G.S., Pen S., Pollard J., Purl V., Reese M.G.,
Ra Mang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ra Milliams S.M., Woododey T., Worley K.C., Wu D., Yang S., Yao O.A.,
Yeben X.H., Zhong F.N., Zhong H., Shith H.O.,
Ra Yell, J.H., Zhong F.N., Zhong H., Wang A.H., Wang Y.,
Ra Yilliams S.M., Woododey T., Worley K.C., Wu D., Yang S., Zho O.A.,
Yeh C., Stept C. B., McTriphy B., McTriphy G., Zhang L.,
The genome Sequence of Drosphila malnogester: ':

C. -1. Sipectolina
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE 2019606; PubMed 10731132;
Adams M.D., Celniker S.E., Hell R.A., Bvans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Wan K.H., Bayley E.M., Marcharley E.M.,
Marcharley E.M., Marcharley E.M., Marcharley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-JUN-2001
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae upf2 protein and upf3 protein (Caenorhabditis elegans SMC-4).*.
Mol. Cell. Biol. 21:209-223(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly)
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EMBL; AF318576; AAG60691.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-7227;
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ilarity 100.0%;
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NUCLEAR (BY SIMILARITY).
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Pred. No. 3.1
0; Mismatches
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Q9A4M2
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Fighter 6; Conserv
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Best Local !
Q9AA21
Q9AA21;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nierman W.C., Feildblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.E., Alley M.R.K., Ohta N., Maddock J.R., Pottocka I., Melson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Deby R.T., Dodson R.J., Durkin A.S., Schinn M.L., Haft D.H., J., Ebry K., Oktonsy J.P., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Uktonsy J.P., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Uktonsy J.P., Tan K., Wolf A., Vannathevan J., Ermolava M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., Shapiro L., Shapiro L., Shapiro L.
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01-JUN-2001
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL. AED05964 ANX44772.1; -.
TIGR, CC2808; -.
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SEQUENCE (
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PRINTS; PRO04047; STROIDFINGER.
SMART; SM00430; HOLI, 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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EMBL; AE003556, AAF50473.1;
HSSP; P03372; IHCP.
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MEDLINE*21173698; PubMed*11259647;
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Pfam; PF00105; zf-C4; 1.
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InterPro; IPR001723; Strdhormone_receptor
InterPro; IPR001628; zf-C4.
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Cell 82:1013-1023(1995).
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                                                                                                                                                                                             MEDLINE-98022869; PubMed-9356176;
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                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96016096; PubMed=7553843;
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                                                                SEQUENCE FROM N.A.
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MEDLINE-21173698;
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                                                                                                          R., Vivancos V., Giangrand is expressed and required 191:118-130(1997).
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RA Mamanatides P.G., Scherer S.E., LIP.W. Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Assburner M., Henderson S.M.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Standon R.C., Rogers Y. H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Adan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Abril J.F., Aphayani A., An H.-J., Andrews-Pfennboch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Belshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bertis K.C., Busam D.A., Boulder H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport D., Dev I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Durbin K.J., Spangelista C.C., Ferraz C., Golhart W.M., Classer K.,
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       A FORSIER C. Gabriellan R. Garg N.S. Gabbart W.M. Glasser K. A Godek A. Goog F. Gorrell J.H., Gu Z. Guan P. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Hernand T.J. Hernandez J.R. Houck J. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. Harris M. H
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EMBL; U34039; AAC46912.1;
EMBL; U81164; AAC47808.1;
TRANSFAC; T02302;
FlyBase; FBgn0014179; gcm.
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001
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Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 GGGTSG
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0 (TrEMBLrel. 13,
1 (TrEMBLrel. 17,
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; GCM_motif.
~<168 MW;
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Pred. No. 3.3e+02;
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genome

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Addams H.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAMADINE J.D., Celliker S.E., Richards S. Ashburner M., Henderson S.N.,
RAMERICAN S.E., RICHARDS S. Ashburner M., Henderson S.N.,
RAMERICAN S.E., RICHARDS S.E., SABDURDER M., Henderson S.N.,
RAMERICAN S.E., RICHARDS S.E., SABDURDER M., Henderson S.N.,
RAMERICAN S.E., RICHARDS S.E., SABDURDER M., Henderson S.N.,
RAMERICAN S.E., ROSPES Y. H.C., ENDAGE S.G., Champe M., Péciféer B.D.,
RAMERICAN S.G., ROSPES Y. H.C., Blazej R.G., Champe M., Péciféer B.D.,
RAMERICAN S.G., ROSPES M., BLAZET R.G., Champe M., Péciféer B.D.,
RAMERICAN S.G., ROSPES M., BANCHER S.G., RAMERICAN S.G.,
RAMERICAN S.G., ROSPES M., BANCHER S.G., ROSPES M.,
RAMERICAN S.G., ROSPES M., BANCHER D., BOCKHEAF N.,
RAMERICAN S.G., BANCHER S.G., BANCHER S.G., CHAMPE B.C.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C., DUNDA P.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C., DUNDA P.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C., DUNDA P.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C., DUNDA P.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C.,
RAMERICAN S.G., ROSPES M., DOWNES M., DUNDAN B.C.,
RAMERICAN S.G., ROSPES M., DOWNES M., PHOCK J.,
RAMERICAN S.G., ROSPES M., DOWNES M., PHOCK J.,
RAMERICAN S.G., ROSPES M., DOWNES M., ROSPESON D.,
RAMERICAN S.G., ROSPES M., RAMERICAN S.G., GLABERT M., ROSPESON D.,
RAMERICAN S.G., ROSPESON D., RAMERICAN S.G.,
RAMERICAN S.G., ROSPESON D., RAMERICAN S.G.,
RAMERICAN S.G., ROSPESON D., RAMERICAN S.G., ROSPESON D.,
RAMERICAN S.G., ROSPESON D., RAMERICAN S.G.,
RAMERICAN S.G., RAMERICAN S.S., ROSPESON D.,
RAMERICAN S.G., RAMERICAN S.S., ROSPESON D.,
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CG13894
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Science
EMBL; AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila
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InterPro; IPR003902; GCM_motif.
SEQUENCE 504 AA; 56202 MW;
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AE003625; AAF52790.1;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
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Pred. No.
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thes 0;
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Matches 6
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01-MAR 2001 (TEMBLICAL 16 Created)

01-MAR 2001 (TEMBLICAL 16 Last sequence update

01-UNI 2001 (TEMBLICAL 17 LAST annotation update

MANDELONITRILE LYASE LIKE POTEIN

ARABIGOPSIS thaliana (House-ear cress):

Bukaryota; Viridiplantae; Streptophyta; endicotyledons; or

Spermatophyta; Magnoliophyta; endicotyledons; or

Spermatophyta; Brassicales; Brassicaceae; Arabidop

enrosids II; Brassicales; Brassicaceae; Arabidop
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
"Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by six physically assigned pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
01-NOV-1998
01-JUN-2001
                                                                       STRAIN-COLUMBIA;
MEDLINE-99087489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDLS.
Prunus serotina (Black cherry).
Brunus serotina (Black cherry).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Rosidae;
                                                                                                 SEQUENCE FROM
                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                           Q9FJ97
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendel; 33024; Pruse;2903;33024.
InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
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Submitted (MAR-1998) to t
Submit, AF053886; AAC61982.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=23207,
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SEQUENCE 528 AA; 59427 MW;
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01-UN-2001 (TREMBLIFE1. 17, Lar.
01-UN-2001 (TREMBLIFE1. 17, Lar.
PTS SYSTEM, LACTOSE-SPECIFIC I.
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Sin S.P., Pilmeaux C., Sezzte S., Suvorov A.M., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
'Complete genome sequence of an M1 strain of Streptococcus pyogenes.'';
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

BMBL, ABD06515; AR34621 J. -
Transferase. Complete proteome.
Transferase. Complete proteome.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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InterPro; IPR000172; GMC_oxred;
Pfam; PF00732; GMC_oxred; 1.
PROSITE; PS00624; GMC_OXRED_2;
   SEOURNCE FROM N.A.
KUTOda M., Oblta T., Uchlyama I., Baba T., Yuzawa
Gul L., Oguchi A., Aoki K.I., Nagai Y., Lian J.,
Matsunatu H., Motryama A., Murakami H., Mosoyama
Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
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Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus
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NCBI_TaxID-158879;
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a A., Mizutani-Ui Y.,
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EMBL APG53885 AMC61981.1 -
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Ogasawara N., Hayashi H., Hiramatsu
"Whole genome sequencing of meticili
aureus.";
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SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids 1; Rosales; Rosaceae; Prunus.
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EMBL; AP003136; BAB43282.1; -
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Voshino C., (
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EMBL. 28084; CAND25561;
Interpo, IPEM03352; PTS_EIIC.
Interpo, IPEM03352; PTS_IIB.
Pfam. PPM03372; PTS_IIB; 1
SEQUENCE 977 AA: 62:367 MM;
      Q9SIN1;
01-MAY-2000
01-MAY-2000
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SEQUENCE FROM N.A.
SCHUITE U., Aign V., Hoheisel J., Branu...
Schuite U., Aign V., Hoheisel J., Branu...
Nyakatura G., Mewes H.W., Mannhaupt G.;
Nyakatura (1.200) to the EMBL/GenBank/DDBJ
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01-OCT-2000
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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STRAIN-ACCC 393 (PILL5-);
STRAIN-ACCC 393 (PILL5-);
MEDLINE-97318691; PubMed-9966115;
Gosalbes M., Monedero V., Alpert C., Perez-Martinez G.;
"Establishing a model to study the regulation of the lactose operon
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-2000 (TrEMBLrel. 15, Last sequence update)
-2001 (TrEMBLrel. 17, Last annotation update)
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ALLÍN X. Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RUILI C.X., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

AR Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Kook H., Moffat K.S.,

Adomin M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

AN Adomis M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

AN Copenhaver G.P., Freuss D., Micrman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Yesquence and analysis of chromosome II of Arabidopsis thaliana.*,

L. Nature 402:761-768(1999).

IN EMBL, AC07087; AND23995.1;

R. Interpro. IPRO14440; TPR. 18

P. Ffam, PPO1515. PPR. 16

P. SMART, SM00018, TPR. 16

P. SMART, SM00018, TPR. 16
                                                                                  Krosky P.M., Underwood M.B., Turk S.R., Feng K.M.+H.,
Ptak R.G., Mesterman A.G., Baron K.K., Townsend L.B.,
Resistance of human cyromegalovirus to benzimidazole
maps to two open reading frames: UL89 and UL35.*,
J. Virol, 72:4721-4728(1998).
EMBL: AF04521, Abc40015.19.
InterPro. IPR002597; Hearpes_env.

SEQUENCE 568 AA; 71154 MR; 049848D7A52596CC CRC64;
                                                                                                                                                                                                                                                                                                                                            056765;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                        Human cytomegalovirus (strain Towne).
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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MEDLINE=98241707; PubMed=9573236;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis,
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Pred. No. 4.5
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Pred. No.
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REALLY 21005600 PURDHESHIZTSSI; YOSHINO M., IICH M., ISHII Y.,

REALLY 21005600 PURDHESHIZTSSI; YOSHINO M., Adachi J., Fekuda S.,

RAR KRANI J. 21005601 PURDHESHIX Y., KONDO M., KONDO S., Zamanaka I.,

RAR ALEKAN T., ILAWA M., NISHI K., KIYOSHWA H., KONDO S., ZAMANAT T., SAITO R.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T., SAITO R.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T.,

RAR KROALTA K., WAISUMA H.A., AARDHINOT M., BRAILOY S., CARAWAT T.,

RAR SAILOT M., STAULLI F., SUKHAITO T., PROJOG G., OOLIVA H.,

RAR GOOTSTEIN M., STAULLI F., SUKHAITO T., ROSOLG G., OOLIVA H.A.,

RAR GOOTSTEIN M., STAULLI F., SUKHAITO T., ROSOLG G., OOLIVA H.A.,

RAR GOOTSTEIN M., STAULLI F., SUKHAITO M., BRAILOR M., GARIYA M., GARIYA M.,

RAR GOOTSTEIN M., BRITCHINOT M., MAZZATELLI J., MODIAL M.,

RAR GOOTSTEIN M., STAULLI J., WAISHIMA J., MAZZATELLI J., MODIAL K.,

RAR WAISHIMA M., GARIYA M., GARIYA M., GARIYA M.,

RAR WAISHIMA M., WAISHIMA J., WAISHIMA J., SAKAMOTO N.,

RAR SARKH H., TOYOCOKA K., WAISH K.H., WAITZ G., WHITLEKER C., MILTLEKE C., WAITLEKE C., W
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O9ASS6:

O1-JUN-2001 (TFEMILIFE1 17, Created)

O1-JUN-2001 (TFEMILIFE1 17, Last sequence update)

O1-JUN-2001 (TFEMILIFE1 17, Last annotation update)

ATG442580/Filaty2.15.

ATG442580/Filaty2.15.

Eukaryota, Varidiplantee, Streptophyta; Embryophyta; Trachcophyta;

Eukaryota, Varidiplantee, Streptophyta;

Eukaryota, Varidiplantee,
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Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J., Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J., Enghet R., Carninci P., Chung H.K., Goldsmith A.D., Hayashizaki Y., Bowser L., Carninci P., Chung H.K., Carlin G., Kawai J., Lam B. Ishida J., Jones T., Kamiya A., Karilin-Reumann G., Kawai J., Lam B. Ishida J., Jones T., Kamiya A., Karilin-Reumann G., Kawai J., Lam B. Lee J.K., Landa M., Narusaka M., Nguyen M., Seki M., Southilok A., Torilmi M., Yamada K., Yu G., Shinozaki K., Davis R.M., Theologis A., Ecker J.R.;

"Arabidopsis cDNA clones.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL. AP367321, AM32908 1.
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01-JUN-2001 (TrEMBLrel.
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Mammalla; Eutheria; Rodentia;
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Pred. No. 4.7e+02
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SMART; SM00370; LRR: 8.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM000369; LRRNT; 1.
SMOUDENCE 809 AA; 80809 MM;
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Q9BJL1;
Q1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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Pfam; PF01463; LRRCT; 1
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EMBL; AK004681; BAB23469.1; -.
MGD; MGI:1914123; 1200009022Rik
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Bogan A., Maina C.V., Yamamotto K., Cohen F., Sluder A.E.;

Bogan A., Maina C.V., Yamamotto K., Cohen F., Sluder A.E.;

Cannoribability elagans nuclear receptor sequences exhibit biophysical

compatability with the ligand-binding domain fold.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF332205; AAX17976.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                 SEQUENCE
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Human mature recep
Human RAGE polypep
Arabidopsis thalia
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                                                                    Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
                                                                                                                                                                                                                                                                                                                                                                             AAM00035 standard; Protein; 156
Phis Invention relates to nucleic acid molecules AAH88706 related from physicontirella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110.
                                                                                                                                                                                                           14-DEC-2000; 2000WO-EP12697
                                                                                                                                                                                                                                                                                                                    Endoxyloglucan transferase sequence #103
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                                         Claim 30;
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                                                                                                                                                                                                                                                                    Physcomitrella
                                                                                                                                                                                                                                                                                      ; carbohydrate metabolism related protein; CMRP; sugar; cofactor; chemical production; carbohydrate; polysaccharide.
                                                                                                           2001-398155/42
DB; AAH88721.
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                                       Page 115; 133pp; English
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related Brevibacteium species and

the genetic engineering of Corynebacterium glutamicum and

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racladed in the invention is a vector containing the CMPP colM. and a host ceal transformed with the vector. The host ceal (a microorganism Corynebacterium or Brevibacterium, moss or algae or a plant ceil) is useful to reproducting a fine chemical such as carbohydrates, cofactors and/or enzymes. The nucleic acid molecules are suitable for modifying a carbohydrate production system in a host, e.g., microorganisms and onzymes lin other. They are also useful to identify those DNA sequences and onzymes in other species which are useful to modify the biosynthesis of starch, ceil wall polysaccharides and sugards. The nucleic acid molecules may be ceil to include the content of t

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                                                                          The present sequence represents a tick salivary gland antigen criated immunogen. The present invention also describes a tick derived series protesse and a tick derived cysteine protesse. A nucleotide sequence encoding any of the above proteins can be used in a wacchie against tick carried infections for domestic animals such as cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tick salivary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                              Claim 2; Page 7; 29pp; Japanese.
                                                                                                                                                                   A gene encoding tick salivary gland antigen - useful as protecting animals from tick-carried infections
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N-PSDB; AAA29614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY90256;
New protein useful for preparation of vaccines for treatment of strangles caused by Streptococcus equi infection, is able to bi mammalian fibronectin -
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                                                                       JACOBSSON K. FRYKBERG L.
                                                                                        LINDMARK H.
                                                        Lindmark H,
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278..279
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255..2
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226..2
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Endoxyloglucan

transferase

sequence #165

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protein of the Invention, designated SFS. SFS binds specifically to mammalian fibronectin or its analogues or fragments. The protein, its analogues or fragments may be used for the preparation of a vaccine that protects horses against strangles (a world-wide distributed and serious disease of the equine upper respiratory tract) caused by 5. equi infection. The antibody and/or antiserum may also be used for the prophylactic or therapetric treatment of 5. equi infection in mammal, especially horses. The use of vaccines containing the fibronectin binding specially horses. The use of vaccines containing the fibronectin binding
                                                                                                                                                                                                                                                                                                                                        Claim
Sequence
                                           protein provides a more effective protection against S. equi infections, with fewer side effects.
                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                                                                         the Streptococcus equi fibronectin binding
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AAM00097
                                                RESULT
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Best Local (
28-SEP-2001
               AAM00097;
                                AAM00097 standard;
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                                                                                      1 GSLGGS
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                                                                                                             Similarity
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 (first entry)
                                Protein;
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Pred. No. 2.4
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W0200144476-A2 Physcomitrella fine chemical carbohydrate metabolism related protein; CMRP; sugar; production; carbohydrate; polysaccharide patens cofactor;

16-DEC-1999; 14-DEC-2000; 2000WO-EP12697 21-JUN-2001 Lerchl J, (BADI ) BASF PLANT Renz A, 99US-0171101 SCI GMBH Ehrhardt Duwenig E H Reindl A, Schmidt R, Cirpus , Reski סי עק

N-PSDB; AAH88783. 2001-398155/42 Freund

Frank M,

?

Bischoff

Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals as a carbohydrates, cofactors and enzymes from microorganisms and plan plants such

Claim 30; Page 127-128; 133pp; English

This invention relates to nucleic acid molecules AAH88706 isolated from physconitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110. Included in the inventions (CMRP) represented in AAM00022 - AAM00110 included in the invention is a vector containing the CMRP CONNA, and a bast cell transformed with the vector. The host cell (a microorganism, Corynebacterium or Brevibacterium, moss or algae or a plant cell) is ceptual for producing a fine chemical such as carbohydrates, cofactors useful for producing a fine chemical such as carbohydrates, cofactors useful for producing a fine chemical such as carbohydrates.

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Best Local
This invention describes a novel nucleic acid (I) containing a sequence that encodes hemocyanin (II) a domain of (I) or its fragment with the immunological properties of at least one domain of (II). The products of the invention have cytostable, virucide, antibacterial, antiparasitic, immunomodulatory and antiparentic activity. (I), and constructs daditionally containing antiper-encoding sequences, are useful in gene therapy of tumors, polypeptides encoded by (I) are useful for treating and carcinoma (of bladder, epithelium, ovary, breast, bronchi or colon-rectum), also hypertension, as vaccines, for treating cocaine misuse and very generally as carriers for pharmaceuticals, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding hemocyanin, and for recombinant production of fus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587517/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Markl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemocyanin, cytostatic; virucide; antibacterial; antiparasitic; immunomodulatory; antihypertensive; gene therapy; tumor; treatent; infection; schiatosomiasis; carcinoma; bladder; epithelium; ovary; breast; bronchi; colon-rectum; hypertension; vaccine; cocaine misus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOS-) BIOSYN ARZNEIMITTEL GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related Brevibactelum species and Acetobacter xylinum and Chlorella to make it a better or more efficient producer of one or more fine chemicals. Mutagenesis of one or more CARPS may also result in CARPS having eltered activities which indirectly impact the production of one or more desired. Activities which indirectly impact the production of one or more desired fine chemicals from plants. Primers AAH80705 - AAH80707 are used in the sequencing of the CARP CDNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1999;
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99DE-1039578.
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ion proteins for vaccination -
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cytostatics. They may also be used to generate antibodics (Ab). Probes based on (I) and Ab are useful for detecting tumor-specific DNA in a cell (by detecting specific binding to cellular DNA or proteins), particularly where associated with the types of cercinoma listed above. Hemocyanins can be produced recombinantly relatively inexpensively and in adequate amounts, eliminating the need to culture gostropods. When used as a carrier, (II) significantly increases the half-life of the attached pharmaceutical, by inhibiting ultrafiltration in the kidneys.
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Length 411;
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390 gslggs 395
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les 6; Conserv
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M. crenulata KLH2 domain c
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                            (first entry)
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tumor; parasite infection; viral infection; antitumor agent; abnormal blood pressure; bladder carcinoma; epithelial carcinoma; ovarian carcinoma; mammary carcinoma; bronchial carcinoma; HtH1; KLH1; carcinoma; cocaine addiction. hemocyanin; cytostatic; vasotropic; vaccine; gene therapy;

Megathura crenulata.

WO200114536-A2

01-MAR-2001

20-AUG-1999; 21-AUG-2000; 2000WO-EP08129

(BIOS-) BIOSYN ARZNEIMITTEL GMBH

Marki Altenhein B, Lieb B, Stiefel

nucleic acid encoding hemocyanin, useful for gene therapy of tumors for recombinant production of fusion proteins for vaccination

Claim 25; Page 133-134; 180pp; German.

This invention describes a novel nucleic acid molecule (N) encoding hemocyanin, a hemocyanin domain or a functional fragment of it with the immunological properties of at least one domain and the immunological properties of at least one domain and the immunological properties of the last one domain and the immunological properties of the immunological properties of the immunological properties of the immunological properties and vasctness or for gene therapy. Compositions comprising nucleic suds of the immunological properties are useful in treating parasite and value fections and as pressure, bladder carcinomas, such in treating parasite and value abnormal months of the immunological properties are useful in treating parasite and value fections and as pressure, bladder carcinomas, such in treating abnormal accommens, overian carcinomas, the manual properties are the properties and value and continuous. It may also è used to cure cocaine

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                                 This invention describes a novel nucleic acid (I) containing a sequence that encodes hemocyanin (II), a domain of (I) or its fragment with the C immunological properties of at least one domain of (II). The products of the invention have cytostatic, virucide, antibacterial, antiparasitic, mununomidiatory and antihypertensive activity. (I) and constructs cadditionally containing antigen-encoding sequences, are useful in gene therapy of tumors polypeptides encoded by (I) are useful for treating c parasitic or viral infections and tumors, particularly schistosomissis and carcinoma (of bladder, pthelium, vary, break, bronchi or colon-rectum), also hypertension, as vaccines, for treating cocalne complete and very generally as carriers for pharmaceuticals, e.g. probes based on (I) and Ab are useful for detecting tumor-specific bhairs cocalne cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab), Probes cytostatics. They may also be used to generate antibodies (Ab) 
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GSLGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid encoding hemocyanin, useful for gene therapy of tumors for recombinant production of fusion proteins for vaccination .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant production
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ilarity 100.0%;
Conservative (
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99DE-1039578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lieb B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stiefel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.6e+02;
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Query Match Best Local Similarity

100.0%;

Score 30; Pred. No.

DB 21; 3.7e+02;

Length 416;

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Sequence

416 AA;

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AAB71157
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Matches
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                                                                                                                                                                                                                         This invention describes a novel nucleic acid molecule (N) encoding hemocyanin, a hemocyanin domain, or a functional fragment of it with the immunological properties of at least one domain of hemocyanin, and which comprises at least one intron is new. The products of the invention have cytostatic and vasotropic activity and can be used in vaccines or for gene therapy. Compositions comprising nucleic acids of the invention are useful in treating tumors. Compositions comprising hemocyanin polypoptide are useful in treating parasite and viral infections and as an antitumor agent it is also useful in treating abnormal blood pressure, bladder carcinomas, epithelial carcinomas, overlan accinomas, namnary carcinomas, pronchial carcinomas, and colon carcinomas. It may also be used to cure cocaine addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor; parasite infection; viral infection; antitumor ejent;
abnormal blood pressure; bladdar carcinoma; epitheial carcinoma;
ovarian carcinoma; mammary carcinoma; bronchial carcinoma;
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                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 159-160; 180pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOS-) BIOSYN ARZNEIMITTEL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1999;
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AAB71157 standard; Protein; 416
                                                                      398 gslggs 403
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                                                                                                1 GSLGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid encoding hemocyanin, useful for gene therapy of tumors for recombinant production of fusion proteins for vaccination \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gslggs 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma; cocaine addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6,
                                                                                                                              Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altenhein
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                                                                                                                                                                                                     416 AA;
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                                                                                                                                            100.0%;
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Pred. No.
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                                                                                                                                  Mismatches
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                                                                                                                                              3.7e+02
                                                                                                                                                            DB 22;
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                                                                                                                                                            Length 416;
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                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence; corn.
                                                                                                                                   18-OCT-2000 (first entry)
            Zea mays subsp. mays
                                                                                                                                                                                                 AAG33306 standard; Protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEM1; KUH1; hemocyanin; cytostatic; vasotropic; vaccine; gene therapy; tumor; parasite infection; viral infection; antitumor agent; abnormal blood pressure; bladder carcinoma; epithelial carcinoma; ovarian carcinoma; mammary carcinoma; bronchial carcinoma;
                                                                                                                                                                                                                                                                             398 gslggs 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid encoding hemocyanin, useful for gene therapy of tumors for recombinant production of fusion proteins for vaccination
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                                                                                                         protein
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ilarity 100.0%;
Conservative (
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                                                                                                   fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              cocaine addiction.
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Pred. No.
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ches 0;
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                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                  06-SEP-2000
                                                                                                                                               termination sequence;
                25-FEB-2000; 2000EP-0301439
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2 gslggs 7
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                                                                                                              mays subsp. mays.
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6; Conser
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                                                                                                                                                                                                                                                                                                                standard; Protein;
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illarity 100.
Conservative
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Pred. No. 3.8e+02;
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9905-015478 9905-0154018 9905-0154079 9905-0155139 9905-0155456 9905-0155459 9905-0156458 9905-0156458	9905-0149929 9905-0149930 9905-0149930 9905-0150884 9905-0151086 9905-0151086 9905-015108 9905-015108 9905-015108 9905-0151303 9905-0151303 9905-0151303 9905-0151303	9918-014589 9918-014704 9918-014704 9918-014704 9918-014702 9918-014703 9918-014703 9918-014703 9918-0148171 9918-0148171 9918-0148841 9918-014864 9918-0149722 9918-0149723	9018-014-632 9018-014-884 9018-014-884 9018-014-808 9018-014-508 9018-014-508 9018-014-508 9018-014-508 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218 9018-014-5218	99US-0143542 99US-0144005 99US-0144005 99US-0144005 99US-0144005 99US-0144325 99US-0144331 99US-0144333 99US-0144333 99US-0144333 99US-0144333

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Best Local
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14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
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21-0CT-1999;
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21-0CT-1999;
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13-OCT-1999;
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26-OCT-1999;
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25-OCT-1999;
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                                                                                                                                                Transferrin binding protein 1; Tbp1; vaccine; antibody; diagnosis;
                                                                                                                                                              Transferrin binding protein 1 gene
                                                                                                                                                                               19-JAN-1997
                                                                                                                                                                                              AAW04867;
                                                                                                                                                                                                             AAW04867 standard; Protein; 931
                                                                                               Peptide
                                                                                                                        Actinobacillus
                                          21-MAR-1996;
                                                        25-SEP-1996
                                                                        EP733708-A2
          (HIPR-) LAB HIPRA SA
                          24-MAR-1995;
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| gslggs 58
                                                                                                                                       pleuropneumonia
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6; Conserv
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                                                                                                                       pleuropneumoniae strain 1371 serotype
                          95ES-0000592
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                                                                                        /label- Sig_peptide
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                    100.0%; 50
100.0%; P
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Pred. No. 4.3
); Mismatches
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thes 0;
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RESULT 1
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Best Local Similarity
Matches 6; Conserva
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production of antibodies useful diagnostically and in universal
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N-PSDB; AAT38071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine against porcine pleuropneumonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat tumour suppressor protein SSeCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1998
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                                                                                           Peptide
                                                                                                                                                  Peptide
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ilarity 100.0%;
Conservative 0;
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757
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785
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202..205
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                                                                                                                                                                                                                                                                                                                                                                                                                                              "encoded by CCC"
                                                                                                                                                                                                                                                       "nuclear localisation
                                                                                                                                                                                                                                                                                                                                                                                       encoded by
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                                                                                                                                "nuclear
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                                                                                                                                                                                       "glycine-rich region"
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Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by GTC.
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                                                                                                                           localisation signal*
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Gaps

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Region

/note- "r

"nuclear

localisation signal.

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"glycine-rich region"

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В
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                                                                                                                                                                                                                                AAW31347
                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises an active truncated form of the novel tumour suppressor protein SSeCKs that is a substrate of protein knows and which acts as a negative regulatory of mitosis and as an alministor of the transformed phenotype. Its amino acid sequence was administer of the transformed phenotype. Its amino acid sequence with the sequence (see AAV0310) obtained from MIN373 cells. The full-length SSeCKs sequence (see AAV0310), as well as provided. Full-length SSeCKs sequence (see AAV0310), as well as provided. Full-seanced by such mucleic acid (see AAV0330), as well as solided proceins encoded by such mucleic acid structure of acids, host cells, and methods of inhibiting the expression of a transformed phenotype in a host cell by introducing the rice acids. Introduction of a SSeCKs nucleic acid or gene product into a host cell in incleic acids. Introduction of a SSeCKs nucleic acid or gene product into a host cell inhibits mitosis of the host cell.

CC aproliferation and/or with the expression of a malignant phenotype. SSeCKs can also be used to treat or identify disorders of comprised the contract of diseases associated with disorders of comprised the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contr
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Best Local
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                     SSECKS; tumour suppressor gene; rat; protein kinase C; mitosis; cancer; malignancy; cell proliferation; Alzheimer's disease;
             therapy
                                                                                              Rat tumour
                                                                                                                               20-JUL-1998
                                                                                                                                                                                                     AAW31347 standard; Protein; 1596 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                          960
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(JAKE/) JAKEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1996;
19-APR-1996;
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                             1 CSLGGS 6
                                                                                                                                                                                                                                                                                                       gslggs
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                                                                                      suppressor protein SSeCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1346 AA
                                                                                                                                                                                                                                                                                                          965
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                            (first entry)
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96US-0635121
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/note "nuclear localisation signal"

1013.1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "zinc finger"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system development.
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                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 18;
Pred. No. 1.3e+03;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 1346;
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                  Secks that is a substrate of protein kinase C and which acts as a constant of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig llA-L; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour suppressor gene SSeCKS - used inhibitor of malignant phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV02302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-535770/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JAKE/) JAKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GELM/) GELMAN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1996;
19-APR-1996;
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1399.1421
"note= "zinc finger"
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96US-0635121
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677..680
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757..760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
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RESULT :
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                      Novel HTDV1 and HTDV2 peptides are disclosed for use in diagn assays for detecting HTDV1 and HTDV2 infection in human sera. Peptides of the invention are given in AAR57055-56.
                                                                                                                                                                                                                                                                                                                               05-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1347 gslggs 1352
 Homo sapiens
              gene therapy;
                                                    06-OCT-2000
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                     HTLV-I and -II peptide(s) and kits contg. them - used to diagnose infection and discriminate between HTLV-I and -II infection
                                                                                                                                                                                                                                                                           WPI; 1994-279743/34
                                                                                                                                                                                                                                                                                                                                              02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                             18-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                           W09418322-A.
                                                                                                                                                                                                                                                                                                                                                                                                        HTLV1; HTLV2; HTLV-I; HTLV-II; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                       HTLV peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR57055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR57055 standard;
                       Human; 5' EST;
                                                                    AAG01209;
                                                                                  AAG01209 standard; Protein; 97
                                                                                                                                                                                                                                     Disclosure; Page 74; 100pp; English.
                                                                                                                                                                                                                                                                                          Fong SKH,
                                                                                                                                                                                                                                                                                                         (GENE-) GENELABS TECHNOLOGIES INC (STRD ) UNIV LELAND STANFORD JUNIO
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
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              chromosome mapping.
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                     expressed sequence tag; secreted protein; cDNA isolation,
                                     protein,
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                                                                                                                                                                                                                                                                                          Hadlock KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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                                                                                                                                                           93.3%;
                                      SEQ ID NO: 5290.
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                                                                                                                                                           Score 28;
Pred. No.
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Pred. No. 1.5e+03;
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                                                                                                                                                     Mismatches
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                                                                                                                                                                          AAG74477
                                                                                                                                                                                RESULT 17
              29-SEP-1999;
03-NOV-1999;
                                                   05-APR-2001
                                                                                 Homo sapiens
                                                                                                colorectal carcinoma
                                                                                                                      Human colon cancer antigen protein SEQ ID NO:5241
                                                                                                                                     03-SEP-2001
                                                                                                                                                    AAG74477;
                                                                                                                                                                  AAG74477 standard;
(HUMA-) HUMAN GENOME SCI INC
                                     28-SEP-2000; 2000WO-US26524
                                                                  WO200122920-A2
                                                                                                       Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                      34 gsiggs
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39

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(first entry)

Protein;

119

990S-0157137 990S-0163280

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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5. ESTS derived from mRNAs encoding secreted proteins. The 5. ESTS were prepared from the lamman RNAs or polyAt RNAS derived from 50 different tissues. EST sequences usually correspond mainly to the 3 untranslated region (UTR) of the mRNA because they are often obtained from onlygo-dT primed CDNA libraries. Such ESTS are not well suited for isolating cDNAs sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included 5' ESTS are derived from mRNAs and genomic DNAs. 5' ESTS are also used in dagnostic, foremic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5'EST) for obtaining conks and genomic DNAs that correspond to 5'ESTS and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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N-PSDB; AAC01215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards
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                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                     regulatory sequences and to design expression and secretion vectors.
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1 GSLGGS 6
                                                                                                                                                                                                  97 AA;
                                                          Conservative
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                                                                                 93.3%;
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                                                          1;
                                                                                     Score 28;
Pred. No.
                                                          Mismatches
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1.9e+02;
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N-PSDB; AAV52611
            WPI; 1998-506734/43
                                             Muller-Cohn J, Narva
                                                                                                         13-MAR-1997;
                                                                                                                                                                       17-SEP-1998
                                                                                                                                                                                                                                 Bacillus thuringiensis.
                                                                                                                                                                                                                                                             HB525 toxin; PCR, primer; amplification; Bacillus lepidoptera; pest; pesticide; Ostrinia nubilalis; Helicoverpa zea; hybridisation.
                                                                                                                                                                                                                                                                                                                                                         02-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW75774 standard; Protein; 633 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                         (MYCO ) MYCOGEN
                                                                                                                                     13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                       Amino acid sequence of lepidoteran-active HD525 toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 6914-6915; 9803pp; English
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Pred. No. 2.4e+02;
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Heliothis virescens;
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This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of ostrinia nublialis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                      Claim 14; Pages 32-34; 50pp; English.
                                                                                                                                                                                                                                                                                                 New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea
Sequence
633 AA;
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Query Match
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Matches 5
1 GSLGGS 6
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349 gsiggs 354
                                          Similarity 83.3
5; Conservative
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                                          Score 28; DB 19;
Pred. No. 1.4e+03;
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RESULT 19
Amino acid sequence of lepidoteran-active 8612 toxin.
                                          02-DEC-1998
                                                                                        AAW75775;
                                                                                                                                AAW75775 standard; Protein; 633 AA
                                       (first entry)
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8612 toxin; Helicoverpa zea; hybridisation epidoptera; PCR; primer; amplification; Bacillus thuringiensis; probe; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;

Bacillus thuringiensis

13-MAR-1998; 17-SEP-1998. 98WO-US05081.

13-MAR-1997; 97US-0040512

WPI; 1998-506734/43. N-PSDB; AAV52612. Muller-Cohn J, (MYCO ) MYCOGEN CORP Narva Æ,

Schnept HE

New insecticidal Bacillus thuringlemsis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa Zea

Claim 5; Pages 36-38; 50pp; English

This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The new sequences, of novel genes polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the novel genes that encode pesticidal and the primers, together with probes derived from the are useful for the identification and characterisation

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RESULT 20
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Best Local Similarity 83.:
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Score 28; DB 21;
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| gsvggs 64
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proteins from various Mycobacterium species microorganisms. The encoding nucleatide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging thouse to the tuberculosis complex. The encoded proteins can be used in vacches for immunisation against a bacterial or viral infection.
                                                                                                                                                                                                                                  Mycobacterial DNA vectors containing reporter constructs - identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                               Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
                                                                                                                                                                                      Claim 32;
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Sequence
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             Similarity 83.
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                   90.0%;
            Score 27; DB
Pred. No. 2e+(
1; Mismatches
                  2e+02;
                          DB 20;
             0
                          Length 67
             Indels
             0
            Gaps
             0;
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AAG27140 standard; Protein; 91 AA.
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Zea mays protein fragment SEQ ID NO: 31861.

(first entry)

termination sequence; Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; corn.

mays subsp. mays.

EP1033405-A2

06-SEP-2000

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Rosen CA,

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14-JAN-2000; 2000US-0176052.
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                    (HUMA-) HUMAN GENOME SCI INC
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13-OCT-1999;
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|gslgga 6
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein sequence encoded by gene 38 SEQ ID NO:130
                                                                                                                                                                                                                                                                                              wound healing; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%;
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Pred. No.
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tches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Sequence

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convolution and manuscriptions of the moderative interference of convolution and the moderative interference of convolutions and the moderative interference of convolutions and convolution in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition provides which are diagnosed or treated include in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include conditions are consistent of the pathological condition. The providers which are diagnosed or treated include catching and contact in the providers of the contact in the contact in the contact in the providers which are diagnosed or treated include attainment diseases, hyperproliferative disorders, carbovascular disorders and providers which are diagnosed or treated include attainment of the contact in the providers which are disported to contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the contact in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The polynucleotide sequences given in AAC8108 to AAC81134 encode the human secreted proteins given in AAB45305 to AAB45357 to AAB45384 represent human secreted polypeptide sequences and proteins bomologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: antiarthritic; Immunosupplessive; antitheumatic; antiprolifigative; expressive; antitheumatic; antiprolifigative;
                                                                        components. AAC8107:
the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 449; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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                                                                        of the present invention.
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AAY59979
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Matches
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                       17-APR-1998;
                                                                                             DE19817948-A1
(META-) METAGEN GES GENOMFORSCHUNG MBH
                                              17-APR-1998;
                                                                                                                    Homo sapiens
                                                                                                                                          treatment; uterine;
                                                                                                                                                     Endometrium; human;
                                                                                                                                                                           Human endometrium tumour EST encoded protein 39
                                                                                                                                                                                                      31-JAN-2000
                                                                                                                                                                                                                             AAY59979;
                                                                                                                                                                                                                                                   AAY59979 standard; Protein; 126
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| 36 gslgga
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5; Conser
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                                                                                                                                                                                                    (first entry)
                       98DE-1017948
                                              98DE-1017948
                                                                                                                                          gene
                                                                                                                                                    tumour; cancer; anticancer;
                                                                                                                                                                                                                                                                                                                                                                     90.0%;
                                                                                                                                      therapy; expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                     Score 27;
Pred. No.
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                                                                                                                                                    cytostatic;
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RESULT
AAB95004
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Matches
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                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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                                                               Ota T, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB95004 standard; Protein; 126 AA
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WPI; 2001-318749/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                            (HELI-)
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                                                               Isogai T,
5, Sugiyama
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence SEQ ID NO:16665
                                                                                                                                                                                                                                                                                                                                                                                          99JP-0248036
                                                               Nishikawa T,
T, Wakamatsu
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Pred. No. 4e+02;
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                                                               Hayashi K,
A, Nagai K,
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                                                               Salto K, Y
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                                                                                                            Yamamoto
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WPI; 1998-179377/16

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AAW53009
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence and an oligonucleotide comprising a sequence, where the polynucleotide which comprises a 3-end sequence, where the combination of oligonucleotide comprises at least 15 nucleotides and the combination of the 5-end sequence/3-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides and gene therapy and particularly full-length cDNAs. The primers are useful for the section and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs. The primers at also weful for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. Anilo165 to Anilo28 and Anilo333 to Anilo742 represent human cDNA sequences; and Anilo29 to Anilo332 and Anilo333 to Anilo332 and anilo acid sequences; and Anilo29 to Anilo332 and Anilo333 to Anilo332 anilo anilo acid sequences; and Anilo329 to Anilo332 and Anilo333 to Anilo332 anilo anilo acid sequences; and Anilo329 to Anilo332 anilo anilo acid sequences; and Anilo329 to Anilo332 anilo anilo acid sequences; and Anilo329 to Anilo333 to Anilo333 to Anilo332 anilo anilo acid sequences; and Anilo332 to anilo acid sequences; and Anilo332 to anilo acid sequences; and Anilo332 to anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anilo acid sequences; anil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length coMns defined in the specification. Whore a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 16665;
                                                                          Chen CMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   T-mfc; inhibitor of MyOD family; treatment; diagnosis; myogenesi
defects; abnormal development; disease; cleidocranial dysplasia;
CDD; rhabdomyosarcoma; muscle tissue cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myogenesis;
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RESULT :
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presence of an I-mf protein or analogue, or for detecting I-mf agonist activity in a test substance. The sequence can be used to treat, model and diagnose defects in myogenesis responsible for ahormal development and disease conditions in mammals including lumens. These include the human disease cleidocranial displasta (CDD), rhabdomyosarcomes and other cancers affecting muscle tissue in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of
development
        AN34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, Sinusitis, purulent ottits media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY3584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; sinusitis; purulent c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Pages
                                                                                                                                                                                                                                04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY35432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY35432 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                        Genome
                                                                                                                                                               WPI; 1999-357842/30
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                                                                                                                                                                                                           (GEST )
                                                                                                                                                                                                                                                                    20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                  W09927105-A2
                                                                                                                                                                                                                                                                                                                                        Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                              vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1999
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 nucleotides
                                                                                                                 Page
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                                                                                                                1213; Disclosure; 1912pp;
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5; Conserv
                                                                                                                                        sequence
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of defects
                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae
                                                                                                                                                                                                                                                                                                                                                                            purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 AA;
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 sequences can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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97FR-0014673
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                                                                                                                                        of Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                      pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane protein
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Pred.
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No.
as immunogenic
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5.2e+02;
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compositions,
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                  19-MAY-1
20-MAY-1
21-MAY-1
24-MAY-1
25-MAY-1
27-MAY-1
28-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein identification; signal transduction pathway; metabolic
hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2000
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46 gtlggs 51
                                                                                                         -MAY-1999;
D-MAY-1999;
L-MAY-1999;
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                                                               -MAY-1999;
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5; Conserv
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9905-012874

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9905-0130007

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Pred. No.
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5.5e+02;
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promoter;
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14719	1473	1470	1463	1459	1459	1459	1452	1451	)1450 )1451	1450	1450	1448	1446	1443	11443	)1443	1443	1440	1440	)1435 )1436	01429	01423	01420	01418	01409	01406 01408	01403	01398	01397	01394	01394 01394	01394	01394	01394	01394	01394	0139	0139	01386	0138
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		28-OCT-1999; 28-OCT-1999;	26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;
		28-OCT-1999; 28-OCT-1999;	26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;
		28-OCT-1999; 28-OCT-1999;	26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;
			26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;
		28-OCT-1999; 28-OCT-1999;	26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;
		28-OCT-1999; 28-OCT-1999;	26-OCT-1999; 28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999; 22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999; 21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	12-OCT-1999;	07-OCT-1999; 08-OCT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	23-SEP-1999;	20-SEP-1999;	15-SEP-1999; 16-SEP-1999;	13-SEP-1999;	07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999;	16-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	09-AUG-1999;	06-AUG-1999;

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C The polynucleotide sequences given in AAC/4337 to AAC/4366 amoode the C human secreted proteins jiven in AAB3481. AAB3481. AAB3482 represent human secreted polyneptide sequences and proteins C hambidgus to them, which are given in the exemption of the present C invention. Human secreted proteins have activities beginned on it he tissues and cells the genes are expressed in Example of activities include: C cytostatic; immunosuppressive; noncropic: maniformetries include: C cytostatic; immunosuppressive; noncropic: maniformetries include: C cytostatic; immunosuppressive; noncropic: maniformetries include: C cytostatic; immunosuppressive; noncropic: maniformetries include: C cytostatic; immunosuppressive; noncropic: maniformetries include: C cytostatic; immunosuppressive; noncropic: maniformetries; and include in antiformetries; and incorpic antiformetries; and incorpic antiformetries; and cytostatic; antiformetries; and incorpic and polynicleotides and polypatides are useful for preventing of amelical condition in e.g. humans, mice, incorpic and also be used as a food additive or preservative to increase or c chromosome identification. They are also useful as probes for diagnosing c candovar ovary cancer may are also useful the system public for condition covary cancer secreted protein useful the system public condition and prevention of (a) cancer (b) families diagnosis; c antiformetries disorders; (d) wand healing; (e) insurediation diseases; and (f) infections diseases such as during the neurological diseases; parasitic infections. AAC74328 to AAC74336 and AAS9401 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 381; 391pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis oncer, immune disorders cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human: secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; nauroprotective; antiviral; antiallargic; heart antidiabetic; anti-inflammatory, antidicer; valerary; anticonvulsant; antibacterial; antifungal; antiparative; condinant; gene therapy; food additive; proservative, chromosome identification; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999; 99US-0126510
07-JAN-2000; 2000US-0174850
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l disease; infectious disease;
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termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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6.1e+02;
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          Score
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6

NO. DB 21; 6.2e+02; 6 Length

192

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74

Matches

RESULT

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RESULT 34
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Matches 5
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                                                                                                                                                                                                                                                                                                                                     for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto A, Dillon DC, Houghton R, Lodes MJ; Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9816646-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW81735;
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an immunogenic portion of a soluble MY antigen which can be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3c; Page 182; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV64530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
  Mycobacterium tuberculosis antigen XP36.
                                 09-NOV-1998
                                                                 AAW64370;
                                                                                            AAW64370 standard;
                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis immunogenic polypeptide XP27 protein #2
                                                                                                                                                                                                  1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:||||
| galggs 79
                                                                                                                                                                    gsvggs 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSLGGS
                                                                                                                                                                                                                               Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical; infection;
                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic; soluble;
                                                                                                                                                                                                                                                                                                         ĄΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0818112
96US-0730510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 196 AA
                                                                                            Protein;
                                                                                                                                                                                                                                              90.0%;
                                                                                                                                                                                                                               Score 27;
Pred. No.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲,
                                                                                            196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; protective immunity; TB; diagnosis.
                                                                                                                                                                                                                                 6.3e+02;
ches 0;
                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                             Length 196;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide is encoded by Mycobecterium tuberculosis antigen XP36 DNA (see AAV4441) that was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. XP36 beers methods and compositions for diagnosing tuberculosis. It provides and compositions for diagnosing tuberculosis. It provides polypeptides (see AAV6421-W64379) comprising an antigenic portion a soluble M. tuberculosis antigen, or an immunogenic portion of M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Mycobacterium tuberculosis polypeptides and DNA - use to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculosis;
                                                                                                         Mycobacterium tuberculosis; M.
                                                                                                                                       M. tuberculosis antigen XP36
                                                                                                                                                                        05-NOV-1999
                                                                                                                                                                                                    AAY39167;
                                                                                                                                                                                                                                 AAY39167 standard; Protein; 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 193-194; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV44421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251292/22.
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                     W09942076-A2
                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA
                                                                              immune
                                                                                                                                                                                                                                                                                                       190 gsvggs
                                                                           mmunotherapy; diagnosis; mmune response; skin test
                                                                                                                                                                                                                                                                                                                                       1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AA
                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; diagnosis; antigen; XP36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis strain Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0818111
96US-0729622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon
                                                                                                                                                                                                                                                                                                                                                                                     90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC, Houghton R,
Twardzik DR, Ve
                                                                                              immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 19;
Pred. No. 6.3e+02;
                                                                                                                                         2nd predicted amino
                                                                                                           tuberculosis; antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 196;
                                                                                                                                         acid sequence.
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ID AAW6
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AC AAW6
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DT 09-N
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Best Local
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                                                                   05-MAY-1998;
18-FEB-1998;
WPI; 1999-527416/44
                             Campos-Neto A,
                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                05-NOV-1999
                   Lodes MJ,
                                                                                                                                         W09942118-A2
                                                                                                                                                             Mycobacterium
                                                                                                                                                                                       Antigen;
                                                                                                                                                                                                                                                                      AAY39024 standard; Protein; 196
                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis. Ag can induce proliferation of or cytokine secretion by. T. B or netural killer cells and/or macrophages to tuberculosis immune subjects. AAZ19249 to AAZ19460 and AAY39083 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY39225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           part of a Mycobacterium tuberculosis antigen (Ag). Also describare vaccines and fusion protein containing M. tuberculosis Ag's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos - Neto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                          190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                        tuberculosis recombinant antigen protein XP36 #2.
                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                           1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                        gsvggs 195
                                                                                                                                                                                                                                                                                                                                 rests
                                                 CORIXA
                                                                                                                                                                              diagnosis;
                                                                                                                                                                                                                                                                                                                                                                Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   are used in
                   Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 177-178; 299pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and protective or therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                               196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                           tuberculosis
                                                 CORP
                                                                   98US-0072596
98US-0024753
                                                                                                99WO-US03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORP.
                  Dillon DC,
SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0072967
98US-0025197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US03268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC,
SG, Skeik
                                                                                                                                                                                       detection;
                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky
                                                                                                                                                                                                                                                                                                                                                                       . 3 %;
                Hendrickson RC, H
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAW, Twardzik
                                                                                                                                                                                      infection; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                       NO.
                                                                                                                                                                                                                                                                                                                                                      DB 2.
6.3e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR,
                Houghton R;
R, Vedvick TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising an immunogenic (Ag). Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                present
                                                                                                                                                                                                                                                                                                                                                                               Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vedvick TS
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                     immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                          Human prostate cancer antigen protein sequence SEQ ID NO:1529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                               13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                               AABS6951
                                                                                                                                                                                                                                                                                                                                                                                                AAB56951 standard; Protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ19119
                                                                                                                                                                                                                                                                                                                                                                                                                                           190 gsvjggs 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 223; 323pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                         prostate cancer; prostate cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA;
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
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83
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                 ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20,
. 6.3e+02;
. ~ 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                        detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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12-MAR-1999; 08-MAR-2000; 2000WO-US05988 21-SEP-2000 WO200055174 - A1 neuroprotective; cytostatic; cardioactive; immunomodulator; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; limmune; reproductive; renal; (HUMA-) Homo ROSE/) gastrointestinal; sapiens. infectious HUMAN ROSEN GENOME C A. 9905-0124270 disease. pulmonary; cardiovascular; proliferative disorder; SCI INC.

disorders such as Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and prostate cancer diagnosis o of f

Rosen

ÇĄ,

Ruben SM

2000-587513/55

AAF16154

Claim Page 1970-1971; 2338pp; English

proteins, called prostate cancer antigens, given in AAB56363 to AAB57302
The prostate cancer antigens can have neuroprotective, cytosteatic,
cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
nephrotropic, antiinfective, gynaecological and antibacterial activities nephrotropic, a and can be used AAF15566 to AAF16505 encode the human prostate cancer associated The prostate cancer antigen

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is family of polypeptides. Host could reflected with a vector comprising the HHHHJ20 nucleic acid are used for the recombinant expression of the polypeptide. The HHHHJ20 nucleic acid may be used as probes or primers to gene, in a patient compared to a healthy individual. This may lead to the concern actoimmune diseases, asthma, rhematoid atthirits, Albeimer's classes, AIDS and stroke, Similarly measuring the amount of the polypeptide in a sample from a patient can be used to diagnose these cidenses. The polypeptide may be used to identify its agonists or content antique to identify membrane-bound or soluble receptors. A cfusion protein of the HHHHJ20 polypeptide and an Igc heavy chain so content action of the HHHHJ20 polypeptide and an Igc heavy chain may be used in therapy, diagnosis and drug screening. The polypucleotide is used content of the HHHHJ20 polypeptide and an Igc heavy chain may be used in therapy, diagnosis and drug screening. The polypucleotide is used content of the HHHHJ20 polypeptide and an Igc heavy chain may be used in therapy, diagnosis and drug screening. The polypucleotide is used to first process the polypucleotide is used.
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AAY06887
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a HWHHJ20 polypeptide, a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albone EF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP911391-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWHHJ20 polypeptide; pim family; cancer; autoimmune disease; asthma; rheumatoid arthritis; Alzheimer's disease; AIDS; stroke; gene therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or research purposes. The prostate cancer antigens may be used disorders such as neural, immune, muscular, reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX32973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 -OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 galggs 107
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 15; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HWHHJ20, useful for diagnosing and treating cancer, AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kikly KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
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97US-0063245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s disease; AIDS; stroke; gene therapy;
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7.6e+02;
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galggs

1 GSLGGS 6

Matches Query Match Best Local

Similarity 5; Conser

Conservative

90.0%;

Score Pred. Mismatches

27; No.

DB 19; 8e+02;

Length 246

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Indels

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Gaps

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Sequence

246

A

protein. Probes from the gene sequence can be used for determining presence of an inf protein or analogue, or for determining against activity in a test substance. The sequence can be used for treatmodel and dispose defects in myogenesis responsible for treatmodel and dispose defects in myogenesis responsible including humans. These includes the human disease collidocranial displasala (CDD), rhabdomyosarcomas and other cancers affering massic tissue in manuals.

Disclosure; Pages 74-75; 92pp; English.

Inhibitor of diagnosis of

MyoD family proteins -defects in myogenesis :

useful for, responsible

for abnormal

e.g. treatment and

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AAW53007
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                                                                                                                              21-AUG-1997;
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                                                                                                                                                                                                                                                             defects;
                                                                                                                                                                                                                                                                                                   Mus musculus I-mfa protein.
                                                                                                                                                                                                                                                                                                                                   03-AUG-1998
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derived from ES
                                                                    (HUTC-) HUTCHINSON CANCER RES CENT FRED
                                                                                                  27-AUG-1996;
                                                                                                                                                                                                                                                       I-mfa; inhibitor of MyoD family; treatment; diagnosis; myogenesis; defects; abnormal development; disease; cleidocranial dysplasia;
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AAW53008
                                                       Query Match 90.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                     The sequence is that of murine I-mfb (inhibitor of MyOD femily) protein. Probes from the gene sequence can be used for determining presence of an I-mf protein or analogue, or for detecting I-mf agonist activity in a test substance. The sequence can be used to treat, model and disaprose defects in myogenesis responsible for abnormal development and disease conditions in mammals, including humans. These include the human disease coldocranial displassia (CDD), rhabdomyosarcomas and other cancers affecting
                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                              development
                                                                                                                                                                                                                                                                                                                                          Inhibitor of MyoD family proteins - useful for, e.g. treatment and diagnosis of defects in myogenesis responsible for abnormal
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N-PSDB; AAV21283.
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.
Fresecan E., Santana M., Schnelder E., Schweizer J., Vertes A.,
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"Bacillus subtills genome profess."
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Mol. Microbiol. 10.377-38 (1993).

10.371-88 (1993).

11. SUBJECT OF ACTIVITY PROTEIN N. PHOSEPHOHISTIDINE + SUGAR PROSENATE...

12. SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

13. SIMILARITY: COMTAINS A PTS EIIC DOMAIN.

14. SIMILARITY: COMTAINS A PTS EIIC DOMAIN.
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Subtilist; BG11348; celB
InterPro; LPRG0352; PfS_EIIC,
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**Microbiology 142:3113-3123(1996).*

-I- PUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUCRAR EMOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOYPRAFTE ACTIVE -TRANSFORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSFERS THE THE DOMAIN CONTAINS THE REMARKE PHOSPHORYLLATION SITE (THE DOMAIN SCHENGHO-HEP). IIA TRANSFERS ITS PHOSPHORYLL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO PHOSPHORYLL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS.
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Miwa Y., Fujita Y.;
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                                                                                         SEQUENCE
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COPE L.D., Hrkal Z., Hansen E.J.;
Detection of phase variation in expression of proteins involved
hemoglobin and hemoglobin-haptoglobin binding by nontypeable
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                                                                                                                                                                                         Outer membrane;
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                                                                                                                                                                                                                                         EMBL; AF221060; AAF80178.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-NTHI N182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Creat
20-AUG-2001 (Rel. 40, Last
20-AUG-2001 (Rel. 40, Last
HEMOGLOBIN BINDING PROTEIN
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Q9KIV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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                   1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                      FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OF THE HUMAN HOST
GSLGGS 179
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                                              Similarity
                                                                                                                                                                                              PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG PS01156; TONB_DEPENDENT_REC_2; 1
                                                                                                                                                                                Repeat.
                                                                                                                                                                                                                               IPR000531; TonB_boxC.
                                      Conservative
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7
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                                                                                                                                                                                       Transport;
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37
29
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                                                                                      113616 MW;
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Pred. No. 1.4
0; Mismatches
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3 X 4 AA TANDEM REPEATS OF Q-P-T-N.
                                                                                                                                                                     POTENTIAL.
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                                                                                   NB BOX.

NB C-TERMINAL BOX.

A551BF3B2C641612
                                                                                                                                                                                     box; Multigene family; Signal;
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                                             DB 1;
1.4e+02;
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RESULT 4
HGP2_HAEIN
                                                                                                                                1- SUBSELULAR LOCATION: OUTER MEMBANE (BY SIMILARITY)

1- MISCELLANDOUS: THIS PROTEIN IS SUBJECT TO PHASE "WATABLE
EXPRESSION ASSOCIATED MITH ALFERNTION IN THE LENGTH OF THE CAA
REPEAT REGION. THIS MCHANISH IS CALLED
ADDITION OR LOSS OF CAA REPEAT UNITS MOULD CHANGE THE READING
ADDITION OR LOSS OF CAA REPEAT UNITS MOULD CHANGE THE READING
ADDITION OR LOSS OF CAA REPEAT UNITS MOULD CHANGE THE READING
FRAME AND RESULT IN IMPROVED TON OF SOP CODONS COUNTRIAN OF THE
FRAME AND RESULT IN IMPROVED TON OF SOME DESCRIPTION OF ANY TO
AVOID THE IMMUNICATION. RESONANCE OF THE HOST USE VANILARITY.

HEMOGLOBEL THIS GAO STOTE TONE DEPENDENT RECEPTOR PROTEIN FAMILY;
1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. THE LEADER PEPTIDE TO
MAXMIZE THE SIMILARITY MITH OTHER ORTHOLOGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                  Unpublished observations (AUG-2001).

1 FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN LEMOGLOBIN COMPLEX OF THE HUMAN FOR HEME UPTAKE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlawage A.R., Bult C.J., Fomb J.F., Dougharty B.A., Mertick J.M., McKenney K., Sutton G., Fitzhugh W., Flelds C.A., Gocayne J.D., Soutt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Heddlom B.C. Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geophagen N.S.M., Brandon R.C., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
20-AUG-2001
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE-20137488; Pubmed-10675023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White O., Clayton R.A.,
Peterson J., Hickey E.,
Submitted (MAY-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Langen H., Takacs B., Evers S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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001 (Rel. 40, Last annotation update)
HEMOGLOBIN AND HEMOGLOBIN-HAPTOGLOBIN
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Dodson R., Gwinn M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision;
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the European Bioinformatics Institute.

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Best Local
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087296;
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PROSITE; PS01156; TONB_DEPENDENT_REC_2: TORD
Outer membrane; Transport; TonB_box; Multigene family; Signal;
                                                                                                                                                       STRAIN-Ela / Serotype B:

Morton D.J., Stull T.L.;

"Conservation of hemoglobin/hemoglobin-haptoglobin binding
Hemophilus Influenzae";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                            HGPB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR;
                                                                                                                                                                                                                                                                        Ren Z., Jin H., Morton D.J., Stull T.L.;
RighB, a gene encoding a second Haemophilus influenzae hemoglobin-
hemoglobin-hatoglobin-binding protein.";
Infect. Immun. 66:4733-4741(1998).
                                                                                                                                                                                                                                                                                                                                                  STRAIN-HI689 /
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Haemophilus.
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                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                STRAIN=H1689 / Serotype B;
MEDLINE=98427137; PubMed=9746572;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
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20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 GSLGGS 195
                                                                   SUBCELLILIAR LOCATION: OUTER MEMBRANE;
MISCELLANEOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE
EXPRESSION ASSOCIATED WITH ALTERATION IN THE LEWSTH OF THE CCAA
REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING.
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                         ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF 'REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A
         REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION WAY TO AVOID THE IMMUNOLOGICAL RESPONSE OF THE HOST
                                                                                                                             HEMOGLOBIN/HAPTOGLOBIN COMPLEX OF FOR HEME UPTAKE.
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HI0661; -.
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6; Conser
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HEMOGLOBIN-HAPTOGLOBIN BINDING
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HAPTOGLOBIN BINDING PROTEIN 2.
7 X 4 AA TANDEM REPEATS OF Q-P-T-N.
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Pred. No.
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BELONGS

TO THE TONB-DEPENDENT

RECEPTOR PROTEIN FAMILY

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Best Local
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20-AUG-2001
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Outer membrane; Transport; TonB box; Multigene family; Signal;
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG
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between the Swiss Institute of Bioinformatics and the Ek
the European Bioinformatics Institute. There are no restr
SEQUENCE FROM N.A
STRAIN-NTHI N182;
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                               NCBI_TaxID-727;
                                          Haemophilus
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                                                                                    BINDING
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annotation updat
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Best Local S
Matches 6
                Coturnix coturnix japonica (Japanese quail).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasiani
                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-NUC-2001 (Rel. 40, Last annotation update)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
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DOMAIN
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                                                                                                           BETA) (LSH-B)
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P45657;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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-I- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                      194 GSLGGS 199
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SUBCELLULAR LOCATION. OUTER MEMBRANE.

MISCELLANSOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE
EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA
REPEAT REGION. THIS MECHANISH IS CALLED SLIPED-STRAND MISPAIRING.
ADDITION OR LOSS OF CCAA REPEAT UNITS GOULD CHANGE THE READING
FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE
REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND
ANY TO AVOID THE INMUNCAGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY:
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ween the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest
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B C-TERMINAL BOX.

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between
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InterPro; IPR001545; Glyco_hormone_beta.
Pfam; PF00007; Cys_knot; 1.
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HSSP; P01233; 1HRP.
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Ouery Match
Best Local S
Matches
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P23758;
01-NOV-1991
01-NOV-1997
20-AUG-2001
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DISULFID
DISULFID
DISULFID
Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
(1)
                          Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Musc
                                                                                                                                       DROME
                                                  Drosophila melanogaster (Fruit fly)
                                                              POX-N
                                                                        PAIRED BOX
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                  Hormone;
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                               GSMGGS 51
                                                                                                                                                                                                                       Similarity 83.
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PS00261; GLYCO_HORMONE_BETA_1; PS00689; GLYCO_HORMONE_BETA_2;
                                                                                                                                                                                                                                                                                                                                                                        Signal; Glycoprotein
1 21
                                                                     (Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
POX-NEURO PROTEIN (PAIRED BOX NE
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166
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BY SIMILARITY.
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Pred. No. 58;
1; Mismatches
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                                                                     BOX NEURONAL
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                                                                                 update)
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                            Brachycera; Muscomorpha.
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RESULT
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Awasaki T. Kimura K.;

Pox.neuro is required for development of che prosophila.";

10 required is 13:707-721(1997).

11 PUNCTION: TRANSCRIPTIONAL REGULATOR THAT

11 PUNCTION: TRANSCRIPTIONAL REGULATOR THAT
                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001523; Paired_box.
Pfam; PF00292; PAX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M86927; AAA28832.1;
EMBL; X58917; CAA41721.1;
PIR; S06951; S06951
HSSP; P06601; IPDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=90059940; PubMed=2573516;
Bopp D., Jamet E., Baumgartner S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92208941; PubMed=1348214;
Dambly-Chaudiere C., Jamet E., Burri M., Bopp
Hafen E., Dumont N., Spielmann P., Ghysen A.,
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                         Paired box: Developmental
                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00027; PAIREDBOX
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SUBCELLULAR LOCATION: NUCLEAR TISSUE SPECIFICITY: CENTRAL A
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                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                           PS00034;
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                                                                                                                           Conservative
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Drosophila.";
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Pred. No. 1.5e
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1.5e+02;
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paired
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                                                                                    RESULT 10
C2AD_BACTU
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Best Local S
Matches 5
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TIGR: HI0729, AC22388.1; -.

TIGR: HI0729, AC22388.1; -.

InterPro; IPR002316; AA_tRNA_Ligase_II.

InterPro; IPR002314; tRNA-synt_2b:

InterPro; IPR002316; tRNA-synt_pro.

Pfam; PP00587; tRNA-synt_2b; 1.

PRINTS; PR01046; TRNASYNTHRO; II.; 1.

PROSTTE: PS00139; AA_TRNA_LIGASE_II_2: FALSE_NEG.

PROSTTE: PS00139; AA_TRNA_LIGASE_II_2: FALSE_NEG.

Aminoacyl-trNA synthetase; Protein blosynthesis; Liv
C2AD_BACTU
Q9RMG3;
20-AUG-2001
20-AUG-2001
20-AUG-2001
PESTICIDIAL
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01-NOV-1995
20-AUG-2001
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SEQUENCE
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McKenney K., Sutton G., Fitzhugh M., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M.,
Weidman J.F., Shillips C.A., Sprijes T., Heddhoum E., Cotton M.D.,
Ulterback T.R., Hanna M.C., Nguyen J.T., Saudek D.M., Brandon R.C.,
Fitchman J.L., Swall K.W., Fraser C.M., Smith H.O.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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P43830;
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MEDLINE-9535050; Pubmed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly influenzae Rd.";
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Bacteria: Proteobacteria:
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                                                                                                                                                                                                 Similarity
5; Conserv
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572 AA;
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SYNTHETASE
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Last sequence update)
Last annotation update,
E (EC 6.1.1.15) (PROLINE--TRNA LIGASE) (PRORS).
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Best Local
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P36096;
01-JUN-1994
01-JUN-1994
15-JUL-1999
                                                                                                                     protein
Yeast 10
[2]
           "The sequ
                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi;
Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                  Saccharomyces corevisiae (Baker's yeast),
Eukaryota, Fungji Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel.
HYPOTHETICAL 87.9
YKL034W OR YKL247
                                                                                                                           Purnelle B., Skala J., van Dyck I., Goffeau A.;
*Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
tRNA gene and four new open reading frames including a leucine zipp
protein and a bomologue to the yeast mitochondrial regulator ABF2.*
*Yeast 10:125-130(1994).
                                                                                                                                                                                                                                    MEDLINE-94262309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the PMBL outstation. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this Statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93127731; PubMed-1481573;
                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BR30;
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Bacteria; Firmicutes; F
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SIMILARITY: BELONGS
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        B., Skala .
Juence of a
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PROTEIN IN PTM-
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                       van Dyck L.,
                                                                                       N.A.
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     fragment on
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Pred.
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PTM-IRX1 INTERGENIC
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Goffeau A.;
n the left arm of yeast chromosome
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2.2e+02;
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Matches 5
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                                                                                                                                                                           Odell C., Churcher C.M., Barrell B.G., Rajandream M.A., Walt
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: THIS MAGRESIUM DEPRINDENT EMEYINE CATALYZES THE
HYDROLYSIS OF AFP COUPLED WITH THE TRANSFORT OF CALCIUM
(BY SIMILARITY).
                                                                                                                                        +++
                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
NCBI_TaxID-4896;
[1]
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01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
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SMART; SM00184; RING; 1.
SMART; SM00184; RING; Transmembrane;
BOTRATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X71622; -; NOT_ANNOTATED_CDS.
EMBL; X69584; CAA49298.1; -.
EMBL; Z8034; CAA61869.1; -.
EMBL; Z8034; CAA61869.1; -.
PIR; S37855; S37855.
SGD: S0001517; YKL034W.
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protein and a homolog of
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SIGNAL
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    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

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(E1-E2 ATPASES). SUBFAMILY IV.
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D TRANSPORTING ATPASE 1
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the UDP-glucose
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MEMBRANE PROTEIN.
ION TRANSPORT ATPASES
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pyrophosphorylase from
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or send a
                                                                              EMBL; Z34288; CAA84056.1; -. EMBL; Z49342; CAA89357.1; -.
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bloinformatics and the DWBL outsit the Buropean Bholiformatics Institute. There are no restrictions use buropean Bholiformatics Institutions as long as its content is In modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                MEDLINE-95282514; PubMed-7762302;
Vandenbol M., Durand P., Dilon C., Portetelle D., Hilger F.;
Vsequence of a 17.1 kb UNA fragment from chromosome X of
Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes: Saccharomycetales: Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                               YUG7_YEAST STANDARD: PRT; 116 AA. P40365; 90 (1. FEB-1955 (Rel. 31, Created) 01-FEB-1955 (Rel. 31, Last sequence update) 15-JUL-1995 (Rel. 36, Last amoutation update) 14POOTHEDICAL 12. YOUAD PROTEIN IN SMC3-MRPLB I YJUG5TW OR J1107 OR HRAI16.
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InterPro; IPR001757; El-E2_ATPase.
InterPro; IPR001454; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
PROSITE: PS00154; ATPASE_E1_E2; 1.
                                                   PIR; S47124; S47124.
SGD; S0003603; YJL067W.
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                                        Hypothetical protein;
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6D5A655ABFA990DF CRC64;
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Matches 5; Conservative
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P20089;
01-FEB-1991
Fani R., Ba
Sgaramella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the EMPL outstation - the EMPL outstation is the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outstation in the EMPL outst
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Drolet M., Zanga P., Lau P.C.K.;
"The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid; relatedness to plasmids REF1010 and pSC101.",
Mol. Microbiol. 4:1381-139(1990).
                                                                                                                                              Bacteria; Pr
Azospirillum
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                      This SNISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outsation the European Bioinformatics institute. There are no restrictions on it use, by non-profit institutions as long as its content is in no was a second of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose of the suppose
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P09397;
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PROSITE; PS00954; IGP_DEHYDRATASE_1;
PROSITE; PS00955; IGP_DEHYDRATASE_2;
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PIR; S16798; S16798.
InterPro; IPR000807; IGPD.
Pfam; PF00475; IGPD; 1.
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EMBL; X61207; CAA43515.1;
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of the ABFH
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ween the Swiss Institute of Bloinformatics and the En
Buropean Bloinformatics Institute. There are no resti
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3-PHOSPHATE = 3-(IMIDAZOL-4-YL)-2-COORBOYD: PHOSENHATE + H(2)O.
PANHMAY: SVENTH STEP IN HISTIDINE BIOSYMTHETIC PATHMAY.
SUPCELLULAR LOCATION: CYTOPLASHIC (BY SIMILARITY) BELONGS TO THE IMIDAZOLEGIZCEROL-PHOSPHATE DEHYDRATASE
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5; Conservative
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207 AA; 226
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BIOSYNTHESIS F
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and

Query Match Best Local Matches

Similarity 5; Conserv

Conservative

90.0%;

Score 27; Pred. No. ;;

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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for convertial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                            MCCoubrey W.K. Jr., Huang T.J., Malnes M.D.;
"Isolation and characterization of a cDNA from the
encodes hemoprotein heme oxygenase-3.";
EUI. J. BLOCHEM. 247.725.732 (1997).
"I PUNCTION: HEME OXYGENASE CLEAVES THE HEME RING
  Heme; Oxidoreductase; Microsome; Multigene family.
DOMAIN 238 243 HRM I (PROBABLE).
DOMAIN 255 260 HRM 2 (POTENTAL).
SEQUENCE 290 AA; 32592 MW; 6600235CE8485829 CR
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O70453;
                                                            Pfam; PF01126; Heme_oxygenase; PROSITE; PS00593; HEME OXYGENA
                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                     EMBL; AF058787; AAC14142.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCoubrey W.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97410004; PubMed-9266719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEME OXYGENASE
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30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S17776; S17776.
Streptomycin biosynthesis
SEQUENCE 281 AA; 31726
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                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE HEME OXYGENASE FAMILY. SIMILARITY: CONTAINS 2 HEME REGULATORY MOTIFS (HRM).
                                                                                                                                                                                                                                                                                                         CO + 3 A + 3 H(2)O.
SUBCELLULAR LOCATION: MICROSOMAL
                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: HEME + 3 AH(2) + O(2)
                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: FOUND IN THE HEART, KIDNEY, BRAIN AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                 METHENE BRIDGE TO FORM BILITWERDIN. BILIVERDIN IS SUBSEQUENTLY CONVERTED OF DELITRIBUL BY BILITERDIN REDUCTARSE. HEME OXYGENASE 3 COULD BE IMPLICATED IN SOME HEME-DEPENDENT RESULATORY ROLE IN THI
                                                        PS00593; HEME_OXYGENASE; 1
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5; Conser
                                                                                    IPR002051; Heme_oxygenase.
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(Rel. 37, Last sequence upd
(Rel. 39, Last annotation u
ASE 3 (EC 1.14.99.3) (HO-3).
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HRM 1 (PRÓBABLE).
HRM 2 (POTENTIAL).
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1; Mismatches
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Query Match
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Matches 5
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30-MAY 2000 (Rel. 39, Last sequence update)
30-MY 2001 (Rel. 40, Last sequence update)
20-MG-2001 (Rel. 40, Last sequence update)
4FPOTHETICAL TRANSCRIPTIONAL REGULATOR RV2282C
RV22B2C OR MT2340 OR MTCY393.28.
Mycobacterium tuberculosis
                                                                                                                   PRINTS; PRO0039; HTHLYSR, PAMILY; 1
PROSTTE; PRO0044; HTHLYSR, PAMILY; 1
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                               EMBL; Z77163; CAB00986.1; -. EMBL; AE007077; AAK46624.1; TIGR; MT2340; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonny J.P., Nelson M.C., Umayam L.A., Ermclaeva M.D., Salzberg S.L
Deloher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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                                                                                                        Hypothetical
Complete prof
                                                                                                                                                                   InterPro; IPRO00847; HTH_LysR
Pfam; PF00126; HTH_1; 1.
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NCBI_TaxID-1773;
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Gene 221:171-177(1998).
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SIMILARITY: BELONGS TO THE HEME OXYGENASE FAMILY.
SIMILARITY: CONTAINS 2 HEME REGULATORY MOTIFS (HRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO + 3 A + 3 H(2)O
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CATALYTIC ACTIVITY: HEME + 3 AH(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUESTRATED AND DESTROYED.
FUNCTION: HEME OXYGENASE 2 COULD BE IMPLICATED OF CARBON MONOXIDE IN BRAIN WHERE IT COULD ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: HEME OXYGENASE CLEAVES THE HEME RING AT THE ALPHA
METHERE BRIDE TO FORM BILLVERDIN BILLVERDIN IS SUBSEQUENTLY
CONVERTED TO BILIRUHIN BY BILIVERDIN REDUCTASE. UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIGHEST IN THE
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                                                                                                                                                                    Oxidoreductase; Microsome; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 PS00593; HEME_OXYGENASE; 1
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(OCT-1997) to the EMBL/GenBank/DDBJ databases.
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          CRC64;
                                                                                                                                                                          (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NI SA
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Query Match Best Local :

Similarity

90

Score Pred.

27; No.

DB 1;

Length 315

밁 8 'n

Gaps

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Matches
                                                                                                                                                                                                                                                                                                                   FOILDERIC SUGGESTING that the two forms of heme oxygenase products of different genes.;

J. BIOL. Cham. 263:3348-3333(1988).

1- PROCTION: HEME OXYGENASE CLEAVES THE HEME RING AT THE METHER BEIDGE TO PORM BILLYEROIM. BILLYEROIM IS SUBSISTENCE TO BILLEUBLIN BY BILLYEROIM REDUCTASE. UNDER HYSTOLOGICAL CONDITIONS, THE ACTIVITY OF HEME OXYGEN HIGHEST IN THE SPLEEN, WHERE SENESCENT ERYTHROCUTES AND THE SPLEEN, WHERE SENESCENT ERYTHROCUTES AND THE SPLEEN.
   EMBL; J05405; AAA41340.1; -. EMBL; U05013; AAA19130.1; -. EMBL; M18918; AAA41347.1; -.
                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the By the Buropean Bioinformatics Institute on There are no restructed by non-profit institutional non as its content modified and this statement is not removed. Usage by an
                                                    or send an email to license@isb-sib.ch)
                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation, characterization, and expression CDNA encoding rat heme oxygenase-2.";
J. Biol. Chem. 265:7501-7506(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88139412; PubMed-3343248; Cruse I., Maines M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Testis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 142-232 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 139:155-161(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The structure, organization and differential expression of the gene encoding rat heme oxygenase-2.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCoubrey W.K. Jr., Maines M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94156193; PubMed-8112599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Testis;
MEDLINE-90237051; PubMed-2185251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HO2_RAT
P23711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rotenberg M.O., Maines M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME OXYGENASE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
                                                                                                                                                                             CO + 3 A + 3 H(2)O.
SUBCELLUIAR LOCATION: MICROSOMAL.
TISSUE SPECIFICITY: MIDELY DISTRIBUTED IN BODY WITH A
CONCEMTRATION IN THE BRAIN.
INDUCTION: HERE OXYGENASE 2 ACTIVITY IS NON-INDUCIBLE
INDUCTION: HERE OXYGENASE 2 ACTIVITY IS NON-INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                     SIMILARITY: BELONGS TO THE HEME OXYGENASE FAMILY.
SIMILARITY: CONTAINS 2 HEME REGULATORY MOTIFS (HRM).
                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: HEME + 3 AH(2) + O(2)
CO + 3 A + 3 H(2)O.
                                                                                                                                                                                                                                                                        FUNCTION: HEME OXYGENASE 2 COULD BE IMPLICATED OF CARBON MONOXIDE IN BRAIN WHERE IT COULD ACT NEUROTRANSMITTER.
                                                                                                                                                                                                                                                                                                              SEQUESTRATED AND DESTROYED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 20, Last sequence update)
. 39, Last annotation updat
(EC 1.14.99.3) (HO-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                       OF HEME OXYGENASE IS
ERYTHROCYTES ARE
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IS SUBSEQUENTLY
                                                                                                       restrictions
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                                                                                                                      collaboration
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Best Local
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Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991
01-AUG-1991
01-NOV-1997
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. It has buropean Bioinformatics Institute on the European Bioinformatics Institute on the European Bioinformatics Institutions on Its use by non-profit institutions as iong as its content is in movey and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(sb-sib.ch).
                                                              EMBL; M57297; AAA26;
EMBL; M57297; AAA26;
PIR; A37845; A37845
                        PDB; 1ESE;
                                                                                                                                                                                                                                        Nat. Struct. Biol.
                                                                                                                                                                                                                                                                  esterase.";
                                                                                                                                                                                                                                                                             "A novel variant of the catalytic triad
                                                                                                                                                                                                                                                                                              Derewenda
                                                                                                                                                                                                                                                                                                      Wei Y., Schottel J.L., Derewenda U.,
                                                                                                                                                                                                                                                                                                                     MEDLINE-95292107; PubMed-7773790;
                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                              scabies."
                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, sequencing, and regulation of expression cextracellular esterase gene from the plant pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                Raymer G., Willard J.M.A., Schottel J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91072254; PubMed=2254271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces scables.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESTERASE PRECURSOR
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A29922; A29922.
PIR; A35199; A35199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GTLGGS
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                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 172:7020-7026(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSLGGS
                                                                                                                                                                                                                       CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR
                                     1ESC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
           Serine esterase;
                          15-OCT-95
                                                 15-OCT-95.
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                                                                             AAA26744.1;
                                                                                        AAA26743.1;
                                                                                                                                                                                                                                          BY ZINC
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35,
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35, Last annotation
(EC 3.1.1.-).
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285
285
146
232
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         Signal; 3D-structure
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Pred. No.
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HRM 2 (POTENTIAL).

QNEPE -> EFRNK (IN REF. 3).

MOI -> TEF (IN REF. 3).

981AADEOIDE1AFCF CRC64;
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RESULT 22

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032445; Q9F
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DISULFID
DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97446530; PubMed-9301118;
Yamano N., Oura N., Wang J., Fujishima S.;
"Cloning and sequencing of the genes for N-scetylglucosamine use
construct divergent operons (nagE-nagAC) from Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NON-O1 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    032445; Q9XTA9;
15-JUL-1998 (Rel. 36, created)
10-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last enoctation update)
N-ACETYLCLUCOSAMINS-6-PHOSPHATE DEACETYLASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
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                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-slb.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAGA OR VC0994
                                                                                                                                                                                                                                                  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
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                        Hydrolase;
                                                                 Pfam; PF02612; NagA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence of both chromosomes
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                                                                                                                                                                                                                                                                                                                                                                                  - D-GLUCOSAMINE 6-PHOSPHATE + ACETATE.
PATHWAY: N-ACETYL GLUCOSAMINE UTILIZATION
SIMILARITY: BELONGS TO THE NAGA FAMILY.
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AE004181; AAF94155.1;
VC0994; -.
                                                                                                            VC0994;
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                     Carbohydrate metabolism; Complete proteome. 79 79 T -> I (IN REF. 1).
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Mismatches 0
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EMBL; X71017; CAA50335.1; A
EMBL; X71018; CAA50336.1; A
EMBL; X71016; CAA50334.1; A
EMBL; X71016; CAA50337.1; A
EMBL; X71019; CAA50337.1; A
PIR; S32007; S32007.
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01-JUN-1994
01-FEB-1996
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PGLR_TOBAC
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                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of a tobacco gene polygalacturonase."; Plant Mol. Biol. 25:283-297(1994).
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01-FEB-1996 (Rel.
POLYGALACTURONASE
                                                                                                                                                             PFGam; PF00295; Glyco_hydro_28; 1. procstme: PS00502; POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                   the
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MEDLINE-94289651; PubMed-8018876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).
Eukaryota: Virdiplantes: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Hagnoliophyta; eudicotyledons; core eudicots;
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                                                            CARBOHYD
                                                                                                                                                                                         InterPro; IPR000743; Polygalacturonase
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                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: POLLEN.
SIMILARITY: BELONGS TO FAMILY 28
(POLYGALACTURONASES).
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FUNCTION: MAY FUNCTION IN DEP
DEVELOPMENT, GERMINATION, AND
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29, Last sequence update)
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PRECURSOR (EC 3.2.1.15) (PG) (PECTINASE)
                                                                                                                                                                                                                                                                                                                      rmatics Institute. There are no resinstitutions as long as its content
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                                                                                                                                                       Signal; Glycoprotein
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Matches 5
                                               amyloid precursor protein.",
Submitted (MAY-1999) to the
[6]
                                                                                           cONA cloning of a novel secreted isoform of the human Receptor for Advanced Glyaction End products (RABB) and characterization of cell co-expressing cell-surface scavenger receptors and Swedish mutant
                                                                                                                                                                                                                                                                                                                                                                                                     Banta A.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C., Elliston K., Stern D., Shaw A.;
"Clouing and expression of a cell surface receptor for advanced glycosylation end products of proteins.";
J. Biol. Chem. 267:14998-15004(1992).
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015109; 015279; 097583; 0942X7;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-NOG-2001 (Rel. 40, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR
(RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                       SEQUENCE
                                                                                                                                                                        Schuler
                                                                                                                                                                                                                                                       submitted (JA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Three genes in the human AHC class III region near the junction with
the class II: gene for receptor of advanced spicosylation end in
products, PBX2 homeobox gene and a notch homolog, human counterpart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGER OR RAGE.
HOMO sapiens (Human).
""arvota; Metazoa; Chordata; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugaya K., Fukagawa T., Matsumoto K., Mita K., Inoko H., Ikemura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMOH
                                                                                                                                                                                                                                                                                     Yamamoto H.;
Molecular heterogeneity of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics
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MEDLINE-95137587; PubMed-7835890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92340547; PubMed-1378843; Neeper M., Schmidt A.M., Brett J.,
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B.I., Futers T.S.;
                                                                                                                                                                  A., Huber G.;
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23:408-419(1994).
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ura H., Migita H., Karasawa J., Y
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--> D (IN CLONES G27W).
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Pred. No. Score 27;

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InterPro; IPR003306, I_d_MIG
InterPro; IPR003500, Ig_C2;
InterPro; IPR003500, Ig_L1k
Pram; PF00047; U_g_L1k
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SMART; SM00408; IG_L1kc; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end-products (RAGE) gene. "
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. The submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. "
PRODUCTS (AGE), THESE ARE NONBEZHATION END AT AN ACCELERATED PROTEINS WHICH ACCUMINATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
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SIGNAL
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Alternative splicing; Polymorphism.
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TISSUE SPECIFICITY: BEDOPHELTAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOCIOBULIN SUPERFAMILY. CONTAINS
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1
ARE PRODUCED BY ALTERNATIVE SPLICING
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
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LIGVILHQRAGRAGERKAFRAGSACELAGGLERGAGS
ESSTGGP -> VSDLEGAARTRAGGANCELAGLARAGNSG
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IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
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Pfam; PF00083; sugar_tr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-97305956; Pubmed-9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
Rhizobiaceae; Rhizobium.
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                 PUTATIVE PURINE PERMEASE YCDG

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PROSITE; PS01116; XANTH_URACIL_PERMASE;
Hypothetical protein; Transmembrane; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000202; AAC74091.1; ALT_INIT. EMBL; D90737; BAA35773.1; -. EMBL; D90738; BAA35783.1; -.
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*A 718-kb DNA sequence of the Escherichia coii K-12 genome

*A 718-kb DNA sequence of the coin region on the linkage man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / MG1655; MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                 Hypothetical
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:137-155(1996).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE)
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NCBI_TaxID=562;
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Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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J. LADIG Res. 36:1305-1314(1995).

1 FUNCTION: MEMBRANE GITCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLOGICENTE ATTENIAL WALLS DURING ATHERCGENESIS. TWO TIPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTORIS OF A DIVERSE GROUP OF MACROALECULES, INCLIDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).

1 SUBUNIT: HONOTRIBER.
1 SUBUNIT: HONOTRIBER.
1 SUBULITATE PRODUCES: 2 150FORMS; I (SHOWN HERE) AND II; ARE PRODUCED BY ALTERNATIVE BELICING.
  EMBL; L04274; AAA39747.1; EMBL; L04275; AAA39748.1;
                                        or send an
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"Structure of the murine macrophage so evaluation of sequences that regulate cell line, P388D.";
                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rateri D.L. Whitman S.C., Block A.E., Daugherty A.; 
"Identification of a functional domain in class A scave that mediates metabolism of AcIDL."; 
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Freeman M., Ashkenas J., Rees D.J., W
Jenkins N.A., Krieger M.;
"An ancient, highly conserved family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 charged macromolecules by macrophage scavenger receptors. . J. Biol. Chem. 268:2126-2133(1993).
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Miyazaki T., Nakamura H., Uesugi S., Imani
Itakura H., Yazaki Y., Matsumoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structures and high and low affinity ligand binding properties of murine type I and type II macrophage scavenger receptors.";
J. Lipid Res. 34:983-1000(1993).
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01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40) Last anoctation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95395388; PubMed-7666008;
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MEDLINE-93131972; PubMed-8380589;
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                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss institute of Bioinformatics and the EM Buropean Bioinformatics institute, where are no restruction by non-profit institutions as ions can be as its content in the content of the swiss of the swisse by and this statement is not removed. Usage by and this statement agreement (See http://www.isb-send an ammail to licenseelsb-sbb.ch).
                                                                                                                                                                                   SIMILARITY: CONTAINS 1 SRCR DOMAIN.
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lia; Eutheria; Rodentia;
ALT_INIT
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Sciurognathi; Muridae;
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te expression in the macrophage
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                                                           (See http://www.isb-sib.ch/announce/
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in class A scavenger receptors
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P54208;
01-OCT-1996
                    Schwarz R., Kaplan A.;
Schwarz R., Kaplan A.;
Schwarz R., Kaplan A.;
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: INVOLVED IN THE LIGHT-INDEPENDENT REDUCTION OF
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LIGHT-INDEPENDENT
(EC 1.3.1.33) (LI
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CARBOHYD
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                                                                                                   Lieman-Hurwitz J.,
                                                                                                                                                 NCBI_TaxID=1140;
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PROSITE; PS50287; SRCR_2; 1.
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MGD; MGI:98257; Scvr.
InterPro; IPR000087; Colla
InterPro; IPR001190; SRCR.
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EMBL; M59445; AAA37464.1;
EMBL; M59446; AAA37465.1;
EMBL; U13873; AAC13774.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00258; SPERACTRCPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01391; Collagen; 1. Pfam; PF00530; SRCR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    346 GSVGGS
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    SIMILARITY)
CATALYTIC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
                                                                                                                                                             ccus sp. (strain PCC 7942) (Anacystis nidulans R2).
Cyanobacteria; Chroococcales; Synechococcus.
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ACTIVITY: CHLOROPHYLLIDE A + NADP(+)
                                                                                                                                                                                                                (LI-POR SUBUNIT N) (DPOR SUBUNIT N)
                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                34, Last sequence update)
40, Last annotation update)
PROTOCHLOROPHYLLIDE REDUCTASE
                                                                                                                                                                                                                                                                  34, Created)
34, Last seq
                                                                                                   Ronen-Tarazi
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MISSING (IN ISOFORM II)
V -> L (IN REF. 3)
N -> K (IN REF. 3)
A -> E (IN REF. 3)
Q -> E (IN REF. 3)
L -> S (IN REF. 3)
L -> S (IN REF. 3)
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Pred. No. 2.6e
1; Mismatches
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COILED COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K2C8_RAT
Q10758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUB-Prostate;
MEDLINE-9212300; PubMed-1370816;
Haleh J.-T., Zhau H.E., Wang X.-H., Liev C.-C., Chung L.W.K.;
Haleh J.-T., Zhau H.E., Wang X.-H., Liev C.-C., Chung L.W.K.;
*Regulation of basal and luminal cell-specific cytokeretin expression
in rat accessory sex organs. Evidence for a new class of androgen-
repressed genes and insight into their pairwise control.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel.
01-NOV-1997 (Rel.
20-AUG-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X57694; CAA47924.1; -.
Photosynthesis; Chlorophyll biosynthesis; Cxldoreductase;
SEQUENCE 466 AA; 51540 MW; 991A91305045574C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTOCHLOROPHYLLIDE + NADPH.
-!- PATHWAY: CHLOROPHYLL BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE CHLM / BCHN FAMILY.
                                                                                         Ando S. Tokul T. Yeno T. Inageki M. Ando S. Tokul T. Yeno T. Inageki M. Protein kinase "Keratin 8 phosphorylation in vitro by cAMP-dependent protein kinase occurs within the amino- and carboxyl-terminal end domains.";

Blochem, Blophys. Res. Commun. 221:67-71(1996)

18 LOCHEM, BLOPHYS. Res. Commun. 221:67-71(1996)

18 LOCHEM, BLOPHYS. RESTORTH KERATIN 18.

18 KERATIN 8 ASSOCIATES WITH KERATIN 18.

19 MICCELLANDOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICCELTAL AND 56-70 KILDOMITONS. RESPECTIVELY).

10 MICCELTAND 56-70 KILDOMITONS. RESPECTIVELY).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                            Wang X., Hsieh J.-T., Zhau H.E.; "Cloning and characterization.of a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KERATIN,
                                                                                                                                                                                                                                                                                   MEDLINE-96220159; PubMed-8660345
                                                                                                                                                                                                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                          Chung-Kuo I Hsueh Ko Hsueh Yuan Hsueh Pao 16:1-7(1994)
                                                                                                                                                                                                                                                                                                                                                          rat prostatic epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95042924; PubMed-7525090;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Last annotation update)
SKELETAL 8 (CYTOKERATIN
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Sciurognathi; Muridae; Murinae; Rat
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P06127;
01-JAN-1988
01-JAN-1988
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DOMAIN
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Jones N.H., Clabby M.L., Dialynas D.P.,
Herzenberg L.A., Strominger J.L.;
"Isolation of complementary DNA clones of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the prop
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PRINTS; PR01276; TYPE2KERATIN
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WEDLINE-91270374; PubMed=1711157;

Van de Velde H., von Hosgen I., Juo W., Parnes J.R

The B-cell surface protein CD72/Lyb-2 is the liga

Nature 351:66-665(1991) A. RECEPTOR IN REGULATING

1- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING

PROLIFERATION CD5 INTERACTS WITH CD72/LYB-2.

1- SUBCELLIARA DCCATTON: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 05, Created)
01-JAN-1988 (Rel. 06, Last sequence update
20-AUG-2001 (Rel. 40, Last annotation update
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIT_MET
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                                                                                                                                                                                                                                                                                                              TISSUE-Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.
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M63482; AAA19668.1; ALT_INIT
S76054; -; NOT_ANNOTATED_CDS
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                                                                                                       PubMed=1711157;
von Hoegen I., Luo W.,
ce protein CD72/Lyb-2
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LINKER 12.
COIL 2.
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EMBL/GenBank/DDBJ databases
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PHOSPHORYLATION (BY SIMILARITY).
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BY SIMILARITY.
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Catarrhini; Hominidae;
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SIMILARITY: CONTAINS 3 Nac. Duilde CD5 entry;
DATABASE: NAME-PROW; NOTE-CD guide CD5 entry;
NWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd5.htm".

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Matches
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last amontation update)
20-AUG-2001 (Rel. 40, Last amontation update)
40, Last amontation update)
Arabidopsis thaliana (Mouse-car cress)
Entaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta, Magnoliophyta; eudicoryledobs; corre eudicotis; Rosidienceae; Arabidopsis.
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EMBL;
STRAIN-CV. COLUMBIA;
Tomlhama T., Shoji K., Hanyu H., Okano T.;
Tomlhama T., Shoji K., Hanyu H., Okano T.;
Submitted (AGC-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON

-i- FUNCTION: RESPONSIBLE FOR THE CORE HISTONES (12A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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A723792B; CCA61584.2;

A723792B; CCA61584.2;

A7237929; CCA61584.2;

A7237930; CCA61584.2;

A7237931; CCA61584.2;

A7237931; CCA61584.2;

A7237932; CAA61584.2;
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"A steroid/thyroid hormone receptor superfamily member in Drosophil 
melanogaster that shares extensive sequence similarity with a 
mammalian homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oro A.E.,
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or send an email to license@isb-sib.ch).
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STRAIN-CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oro A.E., McKeown M., Evans R.M.;

*Relationship between the product
loous and the vertebrate retinoid
Nature 347:298-301(1990).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
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PRINTS; PR01270; HDASUPER
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SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
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0850; Hist_deacetyl; 1.
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501 AA; 56037 N
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                                                                                                                                                                                                                                                      18:4143-4148(1990).
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1; Mismatches
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MEDILINE-2018(011; PubMed-10/731137;

Benos P V. Gatt M K. Asbburner M., Murphy L., Harris D., Cadieu
Benos P V. Gatt M K. Asbburner M., Brun C., Doralbert P., Cadieu
Burrell B G., Perras C., Vidal S., Brun C., Doralbert P., Borkov
Dreano S., Gloux S., Leiaure V., Mottier S., Galibert P., Borkov
Minana B., Kafatos P. C., Louis C., Siden Klamos I., Bolshakov S.
Papagiannakis G., Sponos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Wenrer M., Woutklott P.,

Borkova Cadieu

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STRAIN-OREGON-R; SEQUENCE FROM N.A.

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Amanarides P.C., Schrift C. R., Bouns C.A., Gocayne J.D.,
Amanarides P.C., Schrift S.E., H.C., N., Schilbrane M., Henderson S.N.,
R. Goerge R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Gorge R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Gorge R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
R.A., Berndon G.G., Wortman J.R., Yandell M.D., Zihang Q.C., Chene L.X.,
R.A., Berndon G.G., Wortman J.R., Standard G.C.,
R.A., Martin S.E., Regist S.E., Regist G.C., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Martin S.E., Regist S.E., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Martin S.E., Regist S.E., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Martin S.E., Martin S.E., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Martin S.E., Walson S.E., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Martin S.E., Walson S.E., Hell G., Walson C.R., Miklos G.L.G.,
R.A., Walson S.P., Berman B.P., Bandderl D., Botshakov S.M.,
R.A., Besson K.Y., Benos P.V., Berman B.P., Bandderl D., Botshakov S.M.,
R.A., Bouck J., Bernstein D., Botshakov S.M.,
R.A., Bouck J., Bernstein D., Botshakov S.M.,
R.A., Bottley S., Dahlke C., Davenport L.B., Davide P.,
R.A., Gender D., Bottler A., Dong Z., May R.D., Dev I., Dietz S.M.,
R.A., Doub L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
R.A., Doub L.E., Goreel J.H., G.G., Guan P., Harris M.,
R.A., Gong F., Gorreil J.H., Guz, Guan P., Harris M.,
R.A., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R.A., Houth S.M., Lawrey D., Helman T.J., Hernandez J.R., Houck J.,
R.A., Houth S.M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R.A., Harvey D., Helman T.G., McLeed M.P., Kulp D., Lai Z.,
R.A., Houth S.M., Marsh T.C., McLeed M.P., Melson D.L.,
R.A., Kalmel B.E., Kodira C.D., Kreft C., Kravitz S., Kulp D., Lai Z.,
R.A., Houth S.M., Mushy B., Murphy I., Muzny D.M., Nelson D.L.,
R.A., Kalmel B.E., Kodira G.D., Kreft C., Kredt G.M., Phierson D.,
R.A., Kalmel B.E., Kodira G.D., Kreft C., Kronlard J., Walson B.C.,
R.A., Kalmel B.M., Worlds F.N., Blond M.M.
                                                                                                                                                                                               MEDLINE=94067348; PubMed=8247157;
Yao T.-P., Froman B.M., Jiang Z.,
McKeown M.M., Cherbas P., Evans R
                                                                                                                                                                                                                                                                                                                                    MEDLINE-91007257; PubMed-2120114;
Shea M.J., King D.L., Comboy M.J., Mariani B.D., Kafatos F.C.;
"Proteclas that bind to Drosophila chorion cis-regulatory elements: a
new C2HZ zinc finger protein and a C2C2 steroid receptor-like
                                                                                                                                                                              "Functional
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Science 287:2220-2222(2000).
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Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Talt E.A., Valenti P., Saunders R.D.C.,
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(ECRES) SUCH AS IN THE PROMOTER SUBUNIT: HETERODIMER OF USP AND CAPABLE OF HIGH-AFFINITY BINDING SUBCELLULAR LOCATION: NUCLEAR.
                                                       INSECT METAMORPHOSIS. PLAYS AN POST-EMBRYONIC DEVELOPMENT. BINI (ECRES) SUCH AS IN THE PROMOTER
                                                                                                                    FUNCTION: RECEPTOR FOR ECDYSONE.
                                                                                                                                       366:476-479(1993)
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OF HIGH-AFFINITY BINDING TO ECDYSONE. ULAR LOCATION: NUCLEAR.
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                                                                                                                                                      PRINTS; PR00047; STROIDFINGER PRINTS; PR00398; STRDHORMONER
                                                                                                                                                                            Pfam; PF00104; hormone_rec; 1 Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                FlyBase: FBgn0003964; usp. InterPro; IPR000536; Hormone_rec_lig. InterPro; IPR001723; Strdhormone_reptor. InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                 EMBL; X53379; CAA37459.1;
PIR; A35872; A35872.
PIR; S11513; S11513.
PIR; S13119; S13119.
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                                                                                                           Receptor; Transcription
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SMART; SM00399; ZnF_C4;
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A DNA-BINDING DOMAIN AND A C-TERMINAL STEROLID-BLINDING DOMAIN
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                European
                                                                                                                                                                                                                                                                                                  X52591; CAA36827.1,
AL031765; CAA21122.1; -.
AE003422; AAF45707.1; -.
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Bioinformatics Institute. There a
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RECEPTOR-TYPE.
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RESULT 33
Dudler R.,
Schmidt T.;
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P13562;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequenc
01-NOV-1997 (Rel. 35, Last annotat
TRANSPORT SYSTEM PERMEASE PROTEIN
                              SEQUENCE FROM N.A. MEDLINE-89091146;
                                                                         Mycoplasmataceae;
NCBI_TaxID=2100;
                                                                                                        Mycoplasma hyorhinis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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annotation updat
PROTEIN P69.
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Query Match Best Local S Matches 5

Similarity 5; Conserv

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          HABILS (EPLANTERS SCOUL), "
J. CALL Sci. 107:3133-3144(1994)
-1 FUNCTION: RELEASED EXTRACELLULARLY INTO SEAWATER AND PROVIDES
-1 FUNCTION: RELEASED EXTRACELLULARLY INTO SEAWATER AND PROVIDES
-1 FUNCTION: RELEASED EXTRACELLULARLY INTO SEAWATER AND PROVIDES
-1 FUNCTION OF THE VISCOELASTIC PROPERTIES OF MOCUS.
                                                                                                TISSUE-Slime quand;

MEDLINE-SSA1315; Pubmed-7535307;

KOCH E.A., Spitzer R.H., Pithawalla R.B., Parry D.A.D.;

"An unusual intermediate filament subunit from the cytoskeletal biopolymer released extracellularly into seawater by the primitive
                                                                                                                                                                                                                                                                  Eptatretus stoutii (Pacific hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                 Myxinidae; Eptatretinae;
NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                          THREAD BIOPOLYMER FILAMENT ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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20-AUG-2001
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FUNCTION: PROBABLY PART OF A HIGH-APETINITY TRANSPORT SYSTEM.
SUBCELLILAR LOCATION: INTERAL MEMBRANE PROTEIN (POTENTIAL).
SIMILARITY: HITH HIFERAL MEMBRANE COMPONENTS OF OTHER BINDING.
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. CONTAINS TWO DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; X14140; CAA32358.1;
; M37339; AAA25429.1;
S01830; S01830.
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"AF6921, a novel partner of the MLL gene in t(6:11)(q21:q22),
a forkhead transcriptional factor subfamily.";
Blood 90:3714-3719(1997).
1- PUNCTION: PROBABLE TRANSCRIPTION FACTOR THAT MAY TRIGGERS.
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Bernard O.A.

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M.J., Vlars C.S., Czekay S., C. and characterization of three land three land fixer subfamily.", an FKHR-like gene subfamily.", 47:187-199(1998).

Cavenee W.K., Arden K.C.; e human forkhead genes that

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"Genetic and molecular characterization of essential components
the Vibrio anguillarum plasmid-mediated iron-transport system.",
J. Biol. Chem. 263:2853-2860(1988).
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-1- PTM: PHOSPHORYLATED BY AKT]
-1- DISEASE: INVOLVED IN A T(6:11)(021:023) CHROMOSOMAL TRANSLOCATION
-1- SECOMBARY ACUTE LEMERMA THAT INVOLVES FOXOJA AND MILL.
-1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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Proto-oncogene; Phosphorylation;
ANGNLSYA -> WGKPVYS (IN REP. 2).
BOGKSGKA -> LMGEERK! (IN REP. 2).
S -> T (IN REP. 2).
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LT -> AD (IN REF. 2).
LT -> AD (IN REF. 2).
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RESULT 37
PIGR_RABIT
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                                                                              Mostov K.E., Friedlander M., Blobel G.;
"The receptor for transepithelial transport of IgA and multiple immnoglobulin-like domains.";
Nature 308:37-43(1984).
Frutiger S., Hughes G.J., Hanly \dot{w}.C., Jaton J.-C.; *Rabbit secretory components of different allotypes vary in their
                                  SEQUENCE OF 87-114 AND 410-428,
MEDLINE-88228032; PubMed-3131339;
                                                                                                                                                                                          Oryctologus cuniculus (Rabbit).

Eŭkaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Lagomorpha: Leporidae: Oryctolagus.
                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
POLYMERIC-IMMUNOGLOBULIN RECEPTOR PRECURSOR (POLY-IG RECEPTOR) (PIGR)
                                                                                                                                     MEDLINE=84142246; PubMed=6322002;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               PIGR.
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P01832;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
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Pfam; PF0053; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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EMBL; M34504; AAA79859.1; -.
PIR; B29928; B29928.
PIR; PQ0051; PQ0051.
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*A regulatory gene, angr. of the Iron uptake system of Vibrio
anguillarum; similarity with phage P22 cro and regulation by Iron.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 86:45-51(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UPTAKE SYSTEM OF V.ANGUILLARUM, SUBCELLULAR LOCATION: OUTER MEMBRANE.
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5; Conserv
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TONB C-TERMINAL
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88B67A219395B154 CRC64;
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J. BLOI. Chem. 263:8120-8125(1988)

-1- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
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SMART; SM00410; IG_like;
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SINILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
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J. Biol.
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"DNA sequencing and analysis of a
centromere CERII of Saccharomyces
unknown open reading frames.";
Yeast 8:749-759(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C;
MEDLINE=93070612; PubMed=1441752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROXYACYL-COA TO 3-KETOACYL-COA.
PATHWAY: BETA-OXIDATION PATHWAY:
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: PEROXISOMAL.
DOMAIN: CONTAINS THO SDR DOMAINS.
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FUNCTION: SECOND TRIFUNCTIONAL ENZYME ACTING ON THE BETA-OXIDATION PATHRAXY FOR PATTY ACID. POSSESSING HYDRATASE-DEHYDROCENASE-EPIMERASE ACTIVITIES. CONVERTS FRANS-2-ENOYL-COA VIA D-3-
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InterPro: IPR002347; Adh_short.C2.
InterPro: IPR002539; MaoC_dehydratas.
Pfam; PP00106; adh_short; 2.
Pfam; PP01575; MaoC_dehydratas; 1.
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PROSITE: PS0342; MICROSODIES_CTER; 1.
Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase;
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EMBL; X65124; CAA46243.1; --
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PIR; S25322; S25322.
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-1- SIMILARITY: CONTAINS 1 TENSIN DOMAIN.
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Eur. J. Blochem. 228:297-304(195)
-1- UURCTION: BINDS CLATHRIN HEAVY CHAIN AND PROMOTES ITS ASSEMBLY
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PROSITE; PS50056; TYR_PHOSPHATASE_2; UNKNOWN_1.
PROSITE; PS00636; DNAJ_1; FALSE_NEG.
PROSITE; PS0076; DNAJ_2; 1.
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The European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U09237; AAA79037.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schroeder S., Morris S.A.,
Vinh N.G., Ungewickell E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95220355; PubMed-7705342;
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Mammalia; Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                       Score 27; DB 1; Le
Pred. No. 5.1e+02;
1; Mismatches 0;
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; BC156DC1CF3487FD CRC64;
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20-AUG-2001 BINDING I
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InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation . the European Bioinformatics institute, There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95286263; PubMed-7768598; Elkins C., Chen C.J., Thomas C.E.; "Characterization of the hgbA locus from Haemoobilus ducrevi.";
                                                                              PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG
                                                                                                               Pfam; PF00593; TonB_boxC;
                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus ducreyi.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;

    1 - SUBCELLULAR LOCATION: OUTER MEMBRANE.

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                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY; HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                     ect. Immun. 63:2194-2200(1995).
FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OF
                                                                                                                                                                                                                                                                                                                                                            REQUIRED FOR HEME UPTAKE.
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Total number

Scoring table: Sequence: Title: Perfect score:

Result

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C:Species: Bacillus subtilis

G:Date: 07-Oct-1994 Requence_revision 26-May-1995 #text_change 20-Jun-2000

C:Accession: 33671; G7050

R:Glaser, P.: Kunst, F.; Arnaud, M.; Coudert, M.P.; Gonzales, W.; Hullo, M.F.;
                                                                                                                                                                                                                                   S39671
                                                                                                                                                                           N; Alternate names: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: EMBL:X78974; HID:g475235; PIDN:CAA55572.1; PID:g581673 C;Genetics: A;Start codon: GTG A;Start codon: GTG C;Superfamily: Streptomyces strF protein
                                                                                                                                                                                            phosphotransferase system enzyme II homolog ywbA - Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1994
A;Reference number: S44224
A;Accession: S44230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Streptomyces glaucescens
C:Dato: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-Dec-1999
C:Accession: $44230
R:Mayer, G.: Plepersberg, W.
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C:Superfamily: Aeropyrum pernix hypothetical protein APE0773
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A; Modecule type: DNA
A; Residues: 1-107 < KAW>
A; Cross-reforences: DDBJ: AP000060;
A; Cross-reforences: Strain Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strf protein - Streptomyces glaucescens
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C:Spacles: Aeropyrum pernix
C:Spacles: 10 Aug-1399 isequence_revision 20 Aug-1999 #text_change 20 Jun-2000
C;Accession: G72668
R:Kawarchbysei, Y: Hino, Y: Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takanirahysei, Y: Hino, Y: Horikawa, H.; Yamazaki, S.; Raikawa, Y.; Kudoh, Y.; Yamazaki, J.; P.
DNA Res. 6, 83-101, 199
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy:
A:Reference number: A72450; MUID:99310339
A:Accession: G72668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary
                                    A.; Rapoport, G.; Danchin, A.
ol. Microbiol. 10, 371-384, 1993
                                                                                                                                                                                                                                                                                                                                91 GSLGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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ilarity 100.0%;
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      genome project: cloning and sequencing of the
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Pred. No.
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A;Cross references: GB:299123; GB:AL009126; NID:g2636240; PIDN:CAB15884.1; PID:g26363
A;Experimental source: strain 168
                                          A; Molecule type: DNA
A; Residues: 1-452 <KUN>
                                                                                                                   A:Reference number: A69580; MUID:98044033
A:Accession: F69651
                                                                                         A; Status: preliminary; nucleic acid
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A:Cross-references: EMBL:x73124; NID:g413923; PIDN:cAA51572.1; PID:g413940

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1933

R:Kunst. F: Qasanwara, N.; Moszer; I: Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ebhilch, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-226, 1999

A.; Allohers: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

Lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hölsappel, S.; Hosono, S.; Hullo, M.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

N.; M.; Ogava, K.; Ogavar, A.; Oudega, B.; Patk, S.H.; Patro, V.; Pohl, T.M.; Portete

A; Authors: Schieche, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Schoska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tamahoto, H.; Manne, K.; Yasumoto, V.; V.; Uchiya

A; Mithers: P.; Wapat, A.; Yamamoto, H.; Danne, K.; Yasumoto, V.; Voshida

A; Mithers: P.; Wapat, A.; Yamamoto, H.; Danne, K.; Yasumoto, K.; Yasunoto, V.; Voshida

A; Altors: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A; Accession: 67005.
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A; Residues: 1-444 <KUN>
                                                                                                                                                                                                                      C:Supertamily: phosphotransferase system
C:Keywords: transmembrane protein
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A; Recession: $39671
A; Status; preliminary; nucleic acid sequence not shown; translation
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A; Residues: 1-444 <GLA>
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Matches 6; Conserv
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1 GSLGGS 6
                                                              Conservative
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                                                     Score 30; DE
Pred. No. 1.2
0; Mismatches
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3. 1.2e+02;
0;
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NALEBRIAN BROOKER, A. S. SCHOOLS, F. POLICA, N. S. KURLE, P. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. S. SCHOOLS, S. S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S. SCHOOLS, S.
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sequence not shown; translation

not

A; Gene: NCSP:13E11.260

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C:Supperfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor C:Reywords: iron transport; membrane protein; metal binding; receptor F:1-22/Domain: signal sequence #status predicted <510>
F:23-931/Product: transferrin-binding protein 1 #status predicted <AMT>
F:27-931/Domain: tonB-dependent receptor amino terminal bemology <TNN>
F:27-201/Domain: tonB-dependent receptor amino terminal bemology <TNN>
A:Status: prelininary
A:Molecule type: DNA
A:Rosidues: 1-935 <SCH>
A:Cross-references: EMBL:AL353820: GSPDB:GN00112; NCSP:13E11.260
A:Experimental source: cosmid contig 13E11; strain 74
C:Genetics:
                                                                                                                                                                                                                                      hypothetical protein 1BEL1.560 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Daban M: Medrano, A.; Ouerol E.
Blochem J 115, 287-264, 1996
A:Title: Cloning, sequencing and expression
A:Reference number: S66574; MUID:96207589
A:Accession: S66574
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C;Superfamily: phosphotransferase system enzyme II factor II,
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A: Molecule type: GNA
A: Residues: 1452 GNA
A: Cross references: EMBL: 249992; NID: 9895746; PIDN: CAA90286.1; PID: 9895749
                                                                                                                                  A;Reference number: Z24541
A;Accession: T48778
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A; Accession: S57760
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                                                                                                                                                                             submitted to the Protein
                                                                                                                                                                                               R; Schulte,
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A; Residues: 1-931 <DAB>
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Best Local S
Matches 6
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Best Local Similarity
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Pred. No.
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Pred. No. 2.4e+02;
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                                                                                                                                                                                                        C;Bate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T5:1904 Fischulte, U; Algo, V; Hohelsel, J; Brandt, P; Fartmann, B; Holland, R submitted to the protein Sequence Database, August 2000 A; Reference number: 325858
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                                                                                                                                                                       A; Gene: NCSP:B2:
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Neurospora crassa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                 A; Accession: T51904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein B23111.160 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                               Matches
```

800 GSLGGS 805

1 GSLGGS 6

Similarity 6; Conserv

Conservative

0

100.0%;

Score 30; DB 2; ... Pred. No. 2.8e+02; Pred. No. 2.8e+02;

Length 1051;

0

Gaps

0

1 GSLGGS 6

Similarity 6; Conserv

Conservative

0

Mismatches

0

0

Gaps

0

Holland, R.;

Nyakatu

100.0%;

Score 30; Pred. No.

2.4e+02; B

Length 936; Indels

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-936 < WHI>
A; Cross-references: GB: AE001826;
A; Cross-references: strain R1
                                                                                                                                                                                                                                                                              R:Mhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R., K.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 266, 1971-1577, 1999 the radioresistant bacterium Deinococcus radiodurans R1.
A; Title: Genome, Sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Note: plasmid
                       A; Map position: megaplasmid
A; Genome: plasmid
                                                                                         C; Genetics:
                                                                                                                                                                                                                                       A; Reference number: A75250;
A; Accession: F75622
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Fries 6; Conserve
                                                                        A;Gene: DRB0041
                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Deinococcus radiodurans (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 GSLGGS 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSLGGS 6
   MP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                              MUID: 20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                          NID:g6460827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 2;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                          PIDN:AAF12631.1; PID:g6460927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                              TIGR: DR
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LuceAnizing hormone beta-subunit - quail
C;Species: Coturnix coturnix (quail)
C;Dete: 13-Sep-1996 # sequence_revision 13-Sep-1996 # text_change 16-Jul-1999
C;Abctes: 15.14.2
R;Ando, H; Ishii, S.
Gen. Comp. Endocrinol. 93, 357-368, 1994
A;Title: Molecular cloning of complementary deoxyribonucleic acids for the luralx coturnix japonica).
                                                                                                                                                                                                                                                                                                                                                                                                          A:Molocule type: DNA
A:Residues : 11577 GYL
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AAC24682.1; PID:93002481; GSPDB:GN00
A:Experimental source: strain MROM/TL/81/Friedlin
C:Generics:
A:Gene: STP(1
A:Map position: 1
C:Superfamily: Leishmania major probable membrane protein STPK1
                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable serine/threonine kinase STPKI [Imported] - Leishmania major (strain Friedlin) C:Species: Leishmania major (c:Date: 24-Mar:1999 #sequence_revision 24-Mar:1999 #text_change 19-May:2000 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 C:Accession: 681463; 703859 MID:99178987
     A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RILIN, X.; Nelson, P.J.; Frankfort, B.; Tombler, E.; Johnson, R.; Gelman, I.H.
Mol. Cell. Biol. 15, 2754-2762, 1955
A;Title: Isolation and characterization of a novel mitogenic regulatory gene, 322, which
A;Reference number: A57376; MUID:95257957
A;Reference number: A57376, MUID:95257957
A;Stotus: preliminary; not compared with conceptual translation
A. Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1346 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable regulatory protein 322 - rat (Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Date: 08-Feb-1996 #sequence_revision
C:Accession: A57376
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                         158 GSLGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960 GSLGGS 965
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                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                  Conservative
I51241; MUID:94252550
                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                               4.le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                  Length 1557;
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                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                for the pituitary gly
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                γ
                                                                                                                                                                                                   A:Start codon: GTG
C:Superfamily: Streptomyces strF protein
                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: S44224 A; Accession: S44225
                                                                                                                                                                                                                                                                                                                                                                                                               strf protein - Streptomyces bluensis (fragment)
C;Species: Streptomyces bluensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997
                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-267 <MAY>
                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S44225
R; Mayer, G.; Piepersberg, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
"-+ hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: DNA
A:Residues: 1-252 <BEV>
A:Cross-references: EMB
A:Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 5
A; Note: F8F6.160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z24488
A; Accession: T48422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                        Query Match
Best Local Similarity
Matches 5; Conser
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GSIGGS 159
                                91 GSIGGS
                                                                   1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSLGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GSLGGS 6
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5; Conserv
                                96
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                                                                                                                                                                                                                                                              EMBL: X78972;
                                                                                                                        93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%;
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                                                                                                                                                                                                                                                            NID:g475227; PIDN:CAA55568.1; PID:g581604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                        Score 28; DB 2;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                          April 1994
                                                                                                     Mismatches
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0,

0;

Gaps

0

Length 267;

#text\_change 11-Jan-2000

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R; Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: GB:S70834; NID:g546921; PIDN:AAB30867.1; PID:g546922 C;Superfamily: pituitary glycoprotein hormone beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Accession: 151242
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:MoLecule type; mRNA
A:Residues: 1-166 <AND>
                                                                                                                           EMBL:AL162873
ce: cultivar Columbia; BAC clone F8F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 28; DB
; Pred. No. 1.1e
1; Mismatches
               Score 28;
Pred. No.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
1.1e+02;
               1.7e+02;
                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                              Length 252;
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Indels
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0
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Gaps
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RESULT
E72608
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C:Genetics:
A:Map position: 1
A:Introns: 4BJ; 155/3; 365/3
A:Mote: T1485;7
C:Superfamily: glucose transport protein
C:Keywords: Sugar transport; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable monosaccharidé transport protein 71485,7 - Arabidopsis thaliana C;Beecies; Arabidopsis thaliana (nouse ear cress) C;Date: 01-Fab-1999 #sequence_revision 01-Fab-1999 #text_change 24-Sep-1999 C;Accession: 700450 #text_Change 24-Sep-1999 C;Accession: 700450 #text_Change 24-Sep-1999 C;Accession: 700450 #text_Change 24-Sep-1999 C;Accession: 700450 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-Sep-1999 #text_Change 24-S
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A:Molecule type: DNA
A:Residues: 1-504 <FED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: 214152
A; Accession: T00450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PlyBase:Pox-n
A;Cross-references: PlyBase:FBgn0003130
C;Superfamily: paired box transcription factor Pax-B;
F;5-130/Domain: paired box homology <PBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Note: sequence extracted from NCBI backbone (NCBIN:9997, NCBIN:9991; R:BDPP, D. Jamet, E.; Baumgartner, S.; Burri, M.; Noll, M. EMBO U. 8, 3447-3457, 1989
A:Title: Isolation of two tissue-specific Drosophila paired box genes, A:Reference number; 806950; MUID:90059940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 69, 159-172, 1992
A;Tille: The paired box gene pox neuro: a A;Reference number: A38153; MUID:92208941
A;Accession: A38153
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A; Residues: 1-135 <BOP>
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A:Note: Sequence extracted from NCBH backbone (NCBH:N99907,
R:Boppp D. Jamet, E.: Baumgartner, S.; Burri, M.; Woll, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-425 < DAM>
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Matches 5
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Best Local
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Local Similarity 83.3%;
hes 5; Conservar:...
                                              16
                                                                                                                                                                1 GSLGGS 6
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                                                                                                                                   GSMGGS 38
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AC004260; NID: g3176694; PIDN: AAC34349.1; PID: g3540199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X58917; NID: g8360; PIDN: CAA41721.1; PID: g1405550
                                                                                                                                                                                                                                                                                   93.3%;
                                                                                                                                                                                                                                                                                   Score 28;
Pred. No.
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Pred. No. 2.8e+02;
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3.4e+02;
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                                                                                                                                                                                                                                                                                                            Length 504;
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A.Tille: Complete genome sequence of Pseudomonas aeruginosa PAO1,
A;Reference numbor: A82950; MUID:20437337
A;Accession: C83527
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nes 5; Conserv
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Query Match
Best Local Similarity
Tatches 5; Conserve
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                                                                                                                                                                                                                                                                                     A; Experimental source: strain
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awa, H.; Takamiya, M.; Masudd, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 5, 83-101, 199
A.Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-dun-2000
                                                                                                                                                                                                                                                                                 A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80323.1; PID:g5105009
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-562 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A;Accession: E72608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable hyuB APE1331 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
136 GSIGGS 141
                                            1 GSLGGS
                                            6
                                                                                         Conservative
                                                                                                                 93.3%;
                                                                                         Score 28; DB 2; L
Pred. No. 3.8e+02;
1; Mismatches 0;
                                                                                                                                     Length 562
                                                                                         Indels
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A:Title: Sequence and analysis of chromosome 2
A:Reference number: A84420; MUID:20083487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutator-like transposase [imported] - Arabidopsis haliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A; Residues: 1-569 <STO>
                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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R; Lin, X.; Kaul, S.;
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                                            93.3%;
DB 2;
3.8e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the plant Arabidopsis thaliana
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adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                      prolyl-tRNA synthetase PA0956 [imported] - Pseudomonas aeruginosa (strain PA01)
C;pecies: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83527
                                               R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.;
                                                                                                                                                                                                                                                                                                                       170
                                                   Coulter,
                                               A.L.; Mizoguchi, S.D.;
Coulter, S.N.; Folger,
                                           Hickey,
Larbig,
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an opportunistic

Conservative

Score 28; DB Pred. No. 3.8e 1; Mismatches

Length 569

0,

Gaps

0,

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Cispecies: Bacherichia coli
Cispecies: 30-Sep-1992 #sequence_revision 31-Oct-1997 #text_change 24-Sep-1999
Cipacesidon: B64744; JV0101; JV0061
Cipacesidon: B64744; JV0101; JV0061
R:Blabtherr F. R.; Plankett III. G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I R.A.; Rose 27, D.4; Mou, B.; Shao, Y.
A.A.; Rose 27, D.4; Mou, B.; Shao, Y.
A.Fittle: The Complete genome sequence of Escherichia coli K-12.
A:Rockeronce number: A64720; MUID:97426617
A:Rockersion: B64744; Assession: B64744
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A;Molecule type: DNA
A;Residues: 1-571 <570>
A;Cross-references: GB;AE004529; GB;AE004091; NID:99946851; PIDN:AAG04345.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: pro5; PA0956
C;Superfamily: proline--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Accession: JVIIIO
A.Accession: JVIIIO
A.Molecule type: DNA
A.Residues: 1.25, TV, 28-204, 'Q', 206-572 <ERID
A.Residues: 1.25, TV, 28-204, 'Q', 206-572 <ERID
A.ROSS -references: GB:H97858, NID:y147361, FID:AAA24420.1; FID:g147362
A.ROSE: The sequence from Fig. 2 is inconsistent with that from Fig. 1 in
R. Zibou, 2.; Syvanen, M. 30
B. Bacteriol, 1.72, 281-286, 1990
C64089
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A:MOLECUIE type: DNA
A:MOLECUIE type: DNA
A:RESIGUES: 1-125. (HV', 129-204, 'RPLTNGRCWRR', 217-515, 'RA' <ZHO>
A:CROSS-references: GB.M32357; NID:G145802; PIDN:AMA23710.1; PID:G145803
A:Cross-references: GB.M32357; NID:G145802; PIDN:AMA23710.1; PID:G145803
A:More: the authors identified this protein as global RNA synthesis fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Eriani, G.; Delarue, M.; Poch, O.; Ganglof nature 347, 203-206, 1990
A;Title: Partition of tRNA synthetases into A;Reference number, JV0110; MUID:90370122
                                                                                В
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                                                                                                                                                                                                                                                                 C;Superfamily: proline--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain K-12, substrain MG1655 R;Eriani, G.; Delarue, M.; Poch, O.; Gangloff, J.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000128; GB:U00096; NID:g1786383; PIDN:AAC73305.1;
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A; Residues: 1-572 <BLAT>
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Pred.
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Pred. No. 3.8e+02;
1; M1smatches (
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A; Reference number: Z16450
A; Accession: T08600
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R;Wagner, R.A.; Frie
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C; Superfamily:
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                                          submitted to the EMBL Data Library, August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                       22
                                                               R.A.; Friedman, T.B.; Smith, B.;
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proline--tRNA ligase (EC.6.11.15) - Haemophilus influenzac (strain N,Alternate names; prolyl-tRNA synthetase c.species: Haemophilus influenzae tryine influenzae c.pate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gooayne, J.D.; Scott, J.; Shirley, R.; Llu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.H.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                       C;Superfamily: proline--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-572 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vo.A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd A;Reference number: A64000; MUID:95350630 A;Accession: C64089
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U32756;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; translation not shown
200 GSIGGS
                                                 1 GSLGGS
                                                                                                      Similarity 83. 5; Conservative
205
                                                 6
                                                                                                                                 93.3%;
                                                                                                                                                                                                                                                                                                                                                     GB:L42023; NID:g1573729;
                                                                                                                                 Score 28;
Pred. No.
                                                                                                          Mismatches
                                                                                                                                 3.8e+02
                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 16-Jul-1999
                                                                                                                                                           Length 572;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                         PIDN: AAC22388.1;
                                                                                                              0
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                                                                                                              Gaps
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C;Accession: D85504
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, R;Perna, N.T.; Crotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
Nypothetical protein Opa - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 11-Jun-1999 sequence_revision 11-Jun-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005174; NID:g12512925; PIDN:AAG54496.1; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-572 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: D85504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta
Nature 409, 529-533, 2001
A.;TiLle: Genome sequence of enterohemorrhagic Escherichia
A.;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proline tuak synthetase [imported] - Escherichia coli (strain O157:H7)
C.Specias: Escherichia coli
C.Specias: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
                                                                                                                                                                                             200 GSIGGS 205
                                                                                                                                                                                                                                                 1 GSLGGS 6
                                                                                                                                                                                                                                                                                                     Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                       proline -- tRNA ligase
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83
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Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                      Length 572;
                                                                                                                                                                                                                                                                                                         0
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K.; Apoda
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Wallrath, L.L.; Johnson,

S.; Burnett,

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hypothetical protein F5F19,7 [imported] - Arabidopsis thaliana Cispecies Arabidopsis thaliana (mouse-ear cress) Cispecies (Arabidopsis thaliana (mouse-ear cress) Cipate: 02.Mar-2001 #sequence_revision 02.Mar-2001 #text_change 31-Mar-2001 Ciaccession: 686539 #sequence_revision 02.Mar-2001 #text_change 31-Mar-2001 Ciaccession: 686539 #sequence_revision 02.Mar-2001 #text_change 31-Mar-2001 Ciaccession: 686539 #sequence_revision 02.Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.; Khan, S.; Khaykin, E.; Kim, C.; Alithors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
**Alathors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventos, R.M.
**Alathors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference number, A86141; MUID:21016719

**Accession: 69559**
                  A;Cross-references: GB:AE005173; NID:g4220448; PIDN:AAD12675.1; GSPDB:GN00141C;Genetics:
                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-729 <STO>
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A;MAD position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z24463
A; Accession: T47378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; submitted to the Protein Sequence Database, March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable transposase - Arabidopsis thaliana
N;Alternate names: protein T5C2.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr:2000 #sequence_revision 20-Apr:2000 #text_change 20-Apr:2000
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A;Molecule type: mRNA
A;Residues: 1-654 <WAGD
A;Cross-references: EMBL:AF018078; NID:92394383; PID:92394384
A;Experimental source: strain Oregon-R
C;Genetics:
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A; Residues: 1-675 <OBE>
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Best Local
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Best Local Similarity
Matches 5; Conserv
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
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83.38;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 2; Pred. No. 4.4e+02;
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4.5e+02;
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                                                                                                                                                      A:Molecule type: DNA
A;Residues: 1758 <PUN>
A;Residues: 1758 <PUN>
A;Cross-references: EMBL:Z28034; NID:g486043; PIDN:CAA81869.1; PID:g486044; MIPS:YKLO
A;EXperimental source: strain s288C
R;Purnelle B; Skala, J; van Dyck, L.; Goffeau, A.
Yeast 10, 125-130, 1994
A;Title: Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene
gulator ABF2.
                         A; Molecule type: DNA
A; Residues: 1-758 < PU2>
A; Cross-references:
                                                                     A;Status: nucleic acid sequence not shown
                                                                                                  A; Reference number: S41667;
A; Accession: S41670
                                                                                                                                                                                                                                                                                                                                                                                                       R; Purnelle, B.; Skala, J.; van Dyck, L.; Tettelin, H.; submitted to the Protein Sequence Database, March 1994
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Query Match
Best Local Similarity
Thes 5; Conserv
                                                                            A; Map position: 1
163 GSIGGS 168
                1 GSLGGS
                6
                                Conservative
                                         93.3%;
                                Score 28; DB
Pred. No. 4.96
1; Mismatches
                               . 4.9e+02;
cches 0;
                                                  DB 2;
                                                 Length 729
                               0
                               Gaps
                               0;
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A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schucker, A.; Shine, P.; Southwick, A.M.; S. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; M.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Accession: B86403
C:Accession: B86403
R:Pheologis, A.; Ecker, J.R.; Palm, C.J.; FV
Chin, C.W.; Chung, M.K.; Conn, L.; Conway,
ansen, N.F.; Hujhes, B.; Hulzar, L.
wature 408, 815-820, 2000
A; Map position: 1
                                                                                                  A; Molecule type: DNA
A; Residues: 1-749 <STO>
                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                    A:Reference number: A86141; MUID:21016719
A;Accession: B86403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable mutator-like transposase [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                            GB:AE005172; NID:g10998920; PIDN:AAG26060.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                        Shinn, P.; Southwick, A.M.; Sun, ter, J.C.; Davis, R.W.
                                                        GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                          Khaykin, E.; Kim,
Maiti, R.; Marzia
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hypothetical protein YKU034w precursor - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YKL05
N.Alternate names: hypothetical protein YKL05
C.Species: Saccharomyces cerevisiae
C.Dates: 03-May-1994 #text_change 02-Sep-2000
C.Dates: 03-May-1994 #text_change 02-Sep-2000
C.Dates: 03-May-1994 #text_change 02-Sep-2000
C.McCession: S3785; S1670; S3655
                                                                                                                                                                                                     180 GSIGGS 185
                                                                                                                                                                                                                                                                                    Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                              1 GSLGGS 6
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                           .38
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                                                                                                                                                                                                                                                                                                     Score 28;
Pred. No.
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5e+02;
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Goffeau,

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MUID: 94262309

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A: Map position: IIL
C:Superiamily: Saccharomyces cerevisiae hypothetical protein
C:Superiamily: Saccharomyces cerevisiae hypothetical protein
C:Keywords: transmembrane protein vs. 1616
C:Acywords: transmembrane status predicted cymin protein
C:10-758/product: hypothetical protein vs. 1634 status predicted
C:10-415/Domain: transmembrane status predicted cymin protein
C:10-415/Domain: transmembrane status predicted cymin protein
C:10-617/Domain: transmembrane status protein protein
C:10-617/Domain: transmembrane status protein protein protein
C:10-617/Domain: transmembrane status protein protein
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C:10-617/Domain: transmembrane status protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein prot
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Nature 405, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable heme utilization protein precursor PA1302 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
hypothetical protein rTN22.13 - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress) ("C;Date: 12-reb-1999 #sequence_revision 12-reb-1999 *text_change 18-Aug-2000 ("Accession: T01168
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A: Molacule type: BNA
A: Residues: 1-851 <STOS
A: Cross-references: GB: AE004559; GB: AE004091; NID: 99947228; PIDN: AAG04691.1; GSPDB: GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1.
A; Reference number: A82950; MUID:20437337
A;Accession: A83484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Accession: A83484
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi,
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F; 695-757/Domain:
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A;Experimental source: strain S288C
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A; Residues: 1-570 < PU3>
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A;Tille: The sequence of a 12 kb fragment on the left arm of yeast chromosome XI reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain S288C R;Purnelle, B.; Skala, J.; van Dyck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: PA1302
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                                                                                                                           T01168
                                                                                                                                                             RESULT
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Best Local Similarity
Matches 5; Conserv
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Best Local
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hes 5; Conserv
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transmembrane *status predicted
RING finger homology <RRN>
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1; Mismato
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Pred. No. 5.1e
1; Mismatches
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5.1e+02;
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<TM3>
<TM4>
<TM5>
<TM6>
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C; Superfami
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JE0291
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A;Molecule type: DNA
A;Residues: 1-895 <ROU>
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    FB19 protein - human
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Best Local
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Best Local
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R;Danto, M.
submitted to the EMBL Data Library, April 1
A;Description: The sequence of A. thaliana
A;Reference number: Z14250
A;Accession: 701166
C; Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7
                     A; Map position: 4
A; Introns: 60/1;
A; Note: F7N22.13
                                                                                                                             A. Molecule type: DNA
A. Residues: 1-882 CAND
A. Cross-references: EMBL: ARO55825; NID:g3047060; PID:g3047071
A. Experimental source: cultivar Columbia
                                                                                                                                                                                                                              A; Status: translated from
                                                  230/1; 852/3
                                                                                                                                                                                                                                      GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                   April 1998
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128 GSIGGS 133
               1 GSLGGS 6
                              Similarity
5; Conserv
                              Conservative
                                    93.3%;
                                      Score 28;
Pred. No.
                               Mismatches
                                       5.96+02
                                             В
                               Indels
                               0;
                               Gaps
                               0
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N;Alternate names: hypothetical protein F26C24.7 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24.Mar-1999 #sequence\_revision 24-Mar-1999 Mutator-like transposase (imported) - Arabidopsis thaliana #text\_change 16-Feb-2001

C;Accession: T02597; E84521 R;Bounsity, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998 A;Description: Arabidopsis thalians chromosome II BAC F26C24 genomic sequence.

A; Reference number: Z14680 A; Accession: T02597

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y. M.; Koo, H.; Mcffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, M.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 A; Experimental source: cultivar Columbia A;Cross-references: EMBL:AC004705; NID:g3252804; PID:g3252817 T.P.; Benito, M.I.; Town, C.D.; shen, M.; VanAken, S.E.; Umayam,

of the plant Arabidopsis thaliana

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-895 <STO> A;Cross-references: GB:AE002093; NID:g3252817; PIDN:AAC24187.1; GSPDB:GN00139

A;Gene: At2g14790; F26C24.7

A;Map position: 2 A;Introns: 70/2; 151/1; 292/3; 420/3 C;Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7

129 GSIGGS 134 1 GSLGGS 6 Similarity 5; Conser Conservative 93.3%; Score 28; DB 2; Pred. No. 6e+02; Mismatches 0 Length 895; Indels 0 Gaps

0,

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wichin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansee, N. F.; Hughes, B.; Hultar, L.; A.; Hughes, B.; Hultar, L.; Creasy, anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, A.; Li, J.H.; Ll, Y.; Liu, S., Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khay, R.; Liu, J.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Title: Sequence and analysis of cinconsome 1 of the plant Arabidopsis. A. Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                            probable mutator-like transposase [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
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C;Detc-1958 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Accession: UEO291
R;ToLaTo, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roett Biothem. Biophys. Res. Commun. 250, 555-557, 1998
A;Title: Cloning of a new gene (FB19) within HIA class I region.
A;Reference number: UEO291; MUID:99003493
A;Accession: JEO291
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A;Molecule type: DNA
A;Residues: 1-1028 <570>
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A; Residues: 1-940 <TOT>
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Matches 5; Conserva
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les 5; Conserv
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Pred. No. 6.9e+02;
1; Mismatches 0;
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Pred. No. 6.3e+02;
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Maiti, R
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A; Molecule type: DNA
A; Residues: 1-1127 <57
A; Cross-references: GI
C; Genetics:
A; Map position: 1
                                                                                                         A;Cross-references: EMBL:AF058790; NID:g3722228; PID:g3722229; PIDN:AAC63511.1
                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type; mRNA
A;Residues: 1-1249 «KIM»
                                                                                                                                                                                    A; Title: SynGAP: a synaptic A; Reference number: 217950; A; Accession: T14270
                                                                                                                                                                                                                             C;Accession: T14270
R;Kin, J.H.; Llao, D.; Lau, L.F.; Huganir, R.L.
Neuron 20, 683-691, 1998
                                                                                                                                                                                                                                                                                 Ras-GTPase activating protein SynGAP-b - rat C:Species: Rattus norvegicus (Norway rat) C:Species: 20-Sep-1999 #sequence_revision 20-Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: preliminary; translated from GB/EMBL/DDBJ
A.McLecule type: mRNA
A.Residues: 11166 <SUZ>
A;Cross-references: EMBL:AB016962; NID:d1261311; PID:d1038706; PIDN:CAB19493.1
A;Experimental source: Strain Sprague Dawley
C;Genetics:
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C;Species: Rattus norvegicus (Norway ra
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T13958
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A; Accession: T13958
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1 GSLGGS 6
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                            Score 28; DB 2;
Pred. No. 8.5e+02;
1; Mismatches C
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Pred. No.
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on 20-Sep-1999 #text_change 20-Sep-1999
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7.6e+02;
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7.9e+02;
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C.Accession: T14259

R.Chen, H.J.; Rojas-Soro, M.; Kennedy, M.B.

R.Chen, H.J.; Rojas-Soro, M.; Kennedy, M.B.

R.Chen, H.J.; Rojas-Soro, M.; Kennedy, Pebbuarty 1998

A; Description. A synaptic Ras GTPase-activating protein

A; Raccession: T1425

A; Schuus: pre-liminary; translated from GB/EMBL/DDBJ

A; Stetus: pre-liminary;
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N;Alternate names: protein SynGAP
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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A.Rosledues 1-1293 CCHEA
A;Cross-references: EMBL:AF048976; NID:g2935447; PID:g2935448; PIDN:AAC08071.l
                                                                                                                                                                  A;Title: Sequence of a 17.1 kb DNA fragment from A;Reference number: S50798; MUID:95282514 A;Accession: S50805
                                                                                                                                                                                                                                                                    RESULT 37

S50805

NiAlternate names: hypothetical protein HRAli6; hypothetical protein J1107

C:specios: Saccharomyces cerevisiae

C:specios: Saccharomyces cerevisiae

C:beccios: Saccharomyces cerevisiae

C:beccios: Saccharomyces cerevisiae

C:beccios: 33-01-195; seguence revision 08-Sep-1995 #text_change 29-Oct-1999

C:Accession: S50805; S47124; S56841

R:Vandenboy, M:: Durand, F:: Dion, C.; Portetelle, D.; Hilgor, F.

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A; Introns: 124/3
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A;Resdiues: 1-1402 <0D2>
A;Cross-references: EMBL:667757; NID:91061288; PIDN:CAA91777.1;
A;Experimental source: strain 972h-; cosmid c24B11
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A; Accession: T38339
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submitted to the EMBL Data Library, November 1995
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A; Molecule type: DNA
A; Residues: 1-116 <VAN>
A; Cossidues: 1-116 <VAN>
A; Cossidues: BBBL: Z34288; NID: 9498992;
A; Note: the nucleotide sequence was submitted
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                                                                                                                                    A; Status: nucleic acid sequence not shown;
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Pred. No.
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tches 0;
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A; Residues: 1-149 < DRO>
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R:Vandenbol, M.; Durand, P.; Dion, C.; Porterelle, D.; Hilger, submitted to the EMBL Data Library, June 1994 Appascription: Sequence analysis of a 17.1 kb DNA fragment from A; Reference number: $47117
                                                                                                                                                                                                                                                              A;Cross-references: EMBL: 73.4288; NID: 94.98992; PIDN: CAA84056.1; R:Vandenbol, M.: Durand, P.: Portetelle, D.: Hilger, F submitted to the Protein Sequence Database, September 1995
                                                                                                 A; Map position: 10L
C; Superfamily: Saccharomyces hypothetical protein YJL067w
                                                                                                                                                                                                                      A; Reference number: S56835
A; Accession: S56841
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-116 < VAW>
                                                                                                                                                          A; Cross-references: EMBL: Z49342;
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-116 < POH>
Similarity
5; Conserv
  Conservative
                    90.0%;
                    Score 27;
Pred. No.
                                                                                                                                                             NID:g1008215; PIDN:CAA89357.1; PID:g1008216; MIPS:YJ
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hypothetical protein 5 Thiobacillus ferrooxidans plasmid C:Species: Thiobacillus ferrooxidans C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_ct-C:Accession: S12192 A; Reference number: \$12188; MUID:91125140 A; Accession: \$12192 Mol. Microbiol. 4, 1381-1391, 1990 A; Title: The mobilization and origin of transfer R; Drolet, M.; Zanga, P.; Lau, P.C.K. Mol. Microbiol. 4, 1381-1391, 1990 A; Status: preliminary; translation not shown A;Cross-references: EMBL:X52699 Query Match
Best Local Similarity 83.3
5; Conservative plasmid pTF1 90.0%; ۲, Score 27; Pred. No. Mismatches DB 2; regions #text\_change Length 149 ef. PTF 22 Thiobacillus 0 Gaps ferroox1d8 0;

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Hature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Hitle: Deciphering the biology of Nycobacterium tuberculosis from the complet A;Reference umber: A70500; MUID:98295987

A;Reference umber: A70500; MUID:98295987 A;Status: preliminary; nucleic acid sequence A;Molecule type: DNA hypothetical protein Rv1105 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis (500 tuberculosis) C;Date: 17-Ul-1998 #sequence\_revision 17-Ul-1998 #text\_change 22-Oct-1999 C;Accession: G70897 not shown; translation from the complete not shown

Holroyd,

geno

PIDN:CAA84056.1; to the EMBL Data

Library, June 1994 PID:9499000

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A:cross-references: EMBL:X61207; NID:g38669; PIDN:CAA43515.1; PID:g38670 C;Genetics:
A:Gene: hisb
A:Gene: hisb
C;Superfamily: lmidazoleglycerol-phosphate dehydratase; imidazoleglycerol-phosphate dehyG:Superfamily: lmidazoleglycerol-phosphate dehyG:Reywords: carbon-oxygen lyase; histidine biosynthesis; hydro-lyase
F:36-203/Domain: imidazoleglycerol-phosphate dehydratase homology <IPD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) - Azospirillum brasilense (;Species: Azospirillum brasilense c;Species: Azospirillum brasilense c;Species: Azospirillum brasilense c;Date: 07-un-1990 #text_change 31-War-2000 c;Accession: JE0045; S04399; S16798 R;Pani, R: Bazzicalupo, M; Demiani, G.; Bianchi, A.; Schipani, C.; Sgaramella, V.; Pol Mol, Gen. Genet. 216 224-229, 1989 of Azospirillum brasilense: organization of the ABRY A;Roteschoe number: JE0045; MUID: 89313660 A;Accession: JE0045
Search completed: February 4, 2002, 08:00:55 Job time: 39 sec
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A;Cross-references. GB;AL021897; GB;AL123456; NID;g3256022; PIDN;CAA17221.1; PID;e12519;
C;Experimental source: strain H37kv
C;Genetics;
A;Gene: Rv1105
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A; Residues: 1-207 <FAN>
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                                          SEQUENCE FROM N.A.
STRAIN-BERKELEY;
                                                                                           Drosophila malanogaster (Fruit fly).
Bukaryota: Matazoa; Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota; Diptera: Brachycera: Muscomorpha;
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DNA Res. 6:83-101(1999).
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NCBI_TaxID=7227;
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Pred. No. 55;
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E26C32C0A372D831 CRC64
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Q9pcpl xylella fas
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Q9hq15 halobacteri
Q99jm9 mus musculu
Q9vmz8 drosophila
P70331 mus musculu
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          ayne J.D.,
Galle R.F.,
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RESULT
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Ritton G.C., Wortman J.R., Yandell D., Zhang Q., Chendran B.D.

RA Brandon R.C., Hoptman J.R., Yandell D., Zhang Q., Chendran B.D.

RA Handon R.C., Hoptman J.R., Yandell D., Zhang Q., Chendran B.D.

RA Handon R.C., Hoptman J.R., Hedt C., Rolmburger R., Hiller G.L.G.

RA Handon R.J., Basu A., Vanker G., Hedt C., Rolmburger B.D., Basakey E.N.,

RA Handon R.J., Basu A., Vanker B.D., Hedt C., Rolmburger B.D., Basakey E.N.,

RA Handon R.J., Basu A., Vanker B.D., Hedt C., Bundon B.D., Brettler P.,

RA Handon R.J., Basu A., Vanker B.D., Basakey E.N.,

RA George R.A., Gudy S.N., Dahlke C., Deporter B., Boulettiar P.,

RA George R.A., Basu A., Vanker B.D., Basakey E.N.,

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Q75013;
01-NOV-1996
01-NOV-1996
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Science 287:185-2195(200).
SMALL, ABO03757; AAP56603.1.
FLYBBASE: PSG0009437. CGG6447
SEQUENCE 175 AA; 16827 MM; 96A83146DBF8CBF8 CRC64;
J. Virol. 70:3589-3370(1):
EMBL; U47563; AAB06904.1;
            Tutrol. 70:3589-3598(1996).
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                                                                               HBDINE-98211431; runmeurovoros, MEDDINE-98211431; runmeurovoros, Hill M., Scott W., Wood C. Hutto C., Zhou Y., He J., Geffin R., Hill M., Scott W., Wood C. Congitudinal studies of viral sequence, viral phenotype, and immunologic parameters of human immunodeficiency virus type 1 immunologic parameters of human immunodeficiency virus type 1
                                                                                                                                                   MEDLINE-96211491; PubMed-8648693; Hutto C., Zhou Y., He J., Geffin
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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075018;
01-NOV-1996
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061297;
SEQUENCE FROM N.A. Mulenga A., Sugimoto Submitted (MAY-1998)
                                                                                                                 Haemaphysalis longicornis.

Eukaryotta, Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitlformes, ixodida; Ixodidae; Haemaphysalis.

NCBI_TaxID=44386;
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EMBL; U47568; AABO6909.1; -.
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae;
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RESULT
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Matches
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Best Local S
Matches 6
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"Streptomych Production in Streptomycetes: a Progress I
(In) Baltz R.H., Hegeman G.D., Skatrud P.L. (eds.);
Industrial microorganisms Basic and applied molecular
on 183-194, ASM Press, Herndon (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q54259;
Q54259;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
 Q9VBE0;
01-MAY-2000
                                                                                                                                                                             MEDLINE-96204519: Pubwod-8620209;
Beyer S. Distler J. pispersberg W.;
Beyer S. Distler J. pispersberg W.;
The Str gene cluster for the biosynthesis of 5'-hydroxystreptomycin
in Streptomyces (laucescens GLAL) (ETH 22794); new operons and
evidence for party specific regulation by Str.;
wd. for party 175-784(1996);
EMBL: X10946 (CAASS721);
EMBL: X10946 (CAASS721);
EMBL: X10948 (CAASS721);
EMBL: X10948 (CAASS721);
SEOURCE 281 As: 31477 MM: 11A2C5F4516EBED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Piepersberg W.;
Submitted (JUN-1000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLA 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces glaucescens.
Bacteria; Firmioures; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
                       Q9VBE0
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 13032 (GLA.0);
Retzlaff L., Mayer G., Beyer S.,
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STRAIN-ATCC 13032
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Submitted (APR-1994)
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NCBI_TaxID=1907;
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hes 6; Conserv
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Pred. No.
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Best Loc
Matches
                                Q9X6F4;
Q9X6F4;
Q1-NOV-1999
Q1-NOV-1999
                 FIBRONECTIN
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Enkryota; Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel.
CG6478 PROTEIN.
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Pred. No. 1.7e+02;
; Mismatches 0;
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RESULT
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AC O5
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          09FGC2;
09FGC2;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                     Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl. Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Ottenwalder B., Obermaler B., Tampe J., Haubner D. Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D. Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D. Analysis of 500 Novel Complete Protein Coding Human CDNAs."; EMBL, AL18694; CAB66529.1; "BMBC, AL18694; CAB66529.1; "BYDOLENCE 590 AA; 63303 NW; 1E6B9F2CF44F7014 CDC44.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BQG1;
Q9BQG1;
Q1-JUN-2001
Q1-JUN-2001
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Mammalia; Eutheria;
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DKFZP7610132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibits the binding between fibro Infect. Immun. 67:2383-2388(1999). EMBL; AF136451; AAD29424.1;
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STRAIN-BD3221;
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NCBI_TaxID=1336;
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"SFS, a novel fibronectin-binding
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Primates;
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Pred. No.
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Pred. No.
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HELICASE-LIKE

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RESULT
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Best Local S
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                     Q9AV46;
01-JUN-2001
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01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; ALL17319; CAB55519.1; -.
Hypothetical protein.
SEQUENCE 763 AA; 78737 MW; 819
                                                                                  Q9AV46
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STRAIN-FRIEDLIN;
MEDLINE-98146435; Pubmed-9477341;
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SEQUENCE
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Rajandream M.A., Barrell B.
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major.
Eukaryota; Eugler
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L2903.05.
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheop
Spermatophyta: Magnollophyta: endicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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[abata S.;
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(TrEMBLrel. 13,
(TrEMBLrel. 16,
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Sirel. 13, Last sequence update)
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KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                              Score 30; DB 5;
Pred. No. 5.4e+02;
Mismatches 0;
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Q9AG84;
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Buell C.R., Yuan O., Ouyang S., Moffat K.S., Hill J.N., Burr P.
Hsiao J., Zismann V., Pal G., Bowman C.L., Fujii C.Y., VanAken
Dowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.
Ouackerbush J., White O., Salzberg S.L., Fraser C.M.,
Cryza sativa chromosome 10 BAC OSJNBa0093B11 genomic sequence.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC24594, AKX11344.1;
                                                                                                                                                                                                                                                                                  McCarter L.L., Welsh C., Boles B.,
"The csu Locus of Vibrio parahaemolyticus.",
"The csu Locus of Vibrio parahaemolyticus.",
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AF339087; AAK37523.1,
SEQUENCE 802 AN: B8127 MW: 653711976A2BF37A CRC64;
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01-GENERICAL B.7 KAD PROTEIN.
01/Y2a Seliva (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
permatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bacteria; Proteobacteri
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GONZANEZ G.C., TU R.H., ROSteck P.R. Jr., Schryvers A.B.

GONZANEZ G.C., TU R.H., ROSteck P.R. Jr., Schryvers A.B.

GONZANEZ G.C., TU R.H., ROSteck P.R. Jr., Schryvers A.B.

Foquence, genetic analysis, and expression of Actinoba

picuropneumoniae transferrin receptor genes.';

L. Microbiology 141:2405-2416(1995).

EMBL; U16017, AAC43485.1;

EMBL; U16017, AAC43485.1;

R. EMBL; U16017, TOROB-DAC;

R. FIGHN, PPTONS93, TOROB-DAC;

R. PfGM, PPTONS93, TOROB-DAC;

R. PfGM, PPTONS93, TOROB-DAC;

G. SEQUENCE 898 AA; 102187 MW; 4E49988810A3752A CRC64;
                                                 Q44127;
01-NOV-1996
01-NOV-1996
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Plasmid.
SEQUENCE
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Tieraerztliche Hochschule
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Actinobacillus.
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Plasmid pTF205/023
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NCBI_TaxID=715;
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Pfam; PF00593; TonB_boxC; 1.
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  pleuropneumoniae (Haemophilus pleuropneumoniae).
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NCBI_TaxID=715;
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Q9P6Z0;
01-OCT-2000
01-OCT-2000
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"Sequence, genetic analysis, and expression of Actinobacillus
pleuropheumoniae transferrin receptor genes.";

Microbiology 141:2405-2416(1995),

EMBL; U16019, AAC43497.1.-

EMBL; U16019, AAC43497.1.-

InterPro: IRROUS51; TONB.DOCC.

Pfam: PRO05172; TONB.DOCC.

Pfam: PRO05172; TONB.DOCC.1.

PROSITE: PS01156; TONB.DEPENDENT_REC_2: 1.

PROSITE: PS01156; TONB.DEPENDENT_REC_2: 1.
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PROSITE; PS011;
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"Cloning, sequencing and expression of the transferrin-binding protein
1 gene from Actinobacillus pleuropneumoniae.";
Biochem. J. 315:257-264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 27088;
MEDLINE-96207589; PubMed-8670116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacillus pleuropneumoniae
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                             InterPro; rpR000531; TonB_boxC.
Pfam; pF00593; TonB_boxC; 1.
pROSITE; PS01156; TONB_DEPENDENT_REC_2;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49708; CAA89810.1;
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                                                                                                                                   151 GSLGGS
                                                                                                                                                   1 GSLGGS 6
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6; Conserv
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931 /
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    (TrEMBLrel.
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                                                      PRELIMINARY
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106326
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Last annotation update)
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    Created)
Last sequence update)
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TBP1 GENE.
W; D777366E2FDA54F9 CRC64;
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Pred. No.
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Pred. No.
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                                                      PRT;
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Pasteurellaceae;
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Indels

0, Gaps

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Query Match
Best Local S
Matches 6
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Best Local S
Matches
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01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                           PROSITE; PSO
Hypothetical
SEQUENCE 9
                                                                                                                                                                                                                                               MEDLINE-20036895; PubMed-10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Owlinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vanathevan J.J., Lam P., McDonald L., Ut E.W., Crosby M., Shen M.,
Wanchbevan J.J., Lam P., McDonald L., Minton K.W., Fleischmann R.I
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
Bukaryota: Fungi; Ascomycota: Pezizomycotina;
Sordariales; Sordariaceae: Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                               Science 286:1571-1577(1999).
EMBL; AE001826; AAF12631.1;
                                                                                                                                                                                                                "Genome sequence of the radioresistant radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRB0041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RZS3
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SWART; SM00355; ZnE_C2H2; 2
PROSITE: PS00026; ZINC_FINGER_C2H2_1; 2
PROSITE: PS0157; ZINC_FINGER_C2H2_2; 2
DNA-Thidling, Metal-binding; Zinc-finger
SEQUENCE 935 AA; 103980 MM; 35F0F646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMEMBL; AL353820; CAB88594.1; -. InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Schulte U., Aign V.,
Nyakatura G., Mewes
                                                                                                                                                                TIGR; DRB0041
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid MP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus radiodurans
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                                                                                                                                             InterPro; IPR002173; PfkB
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       Similarity
6; Conserv
                                                                                        PS00583; PFKB_KINASES_1;
ical protein; Plasmid; Com
936 AA; 97723 MW; 4AE
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6; Conser
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hilarity 100.
Conservative
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H.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ
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    17, Last annotation update)
PROTEIN.

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                   Score 30;
Pred. No.
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Pred. No. 6.9
); Mismatches
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4A8D433D7F1495C0
       Mismatches
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6.9e+02;
0;
                                                                                                                                                                                                                               bacterium
                     DB 2;
6.9e+02;
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                                   Length 936;
                                                                                        CRC64;
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       Indels
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    0;
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Best Local
              Ren Z., Jin H., Morton D.J., Stuil T.L.;

*hypB, a gene encoding a second Heemophilus in hemoglobin hattoglobin-binding protein.*;

Infect, Immun. 66;4733-474(1998).

InterPo. 1PROUSSII. FORB_boxC.
InterPo. 1PROUSSII. FORB_boxC.
InterPo. 1PROUSSII. FORB_boxC.
PORSITE, PS002155 MITCOH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                             087296
087296;
01-NOV-1998
01-NOV-1998
01-JUN-2001
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=HI689 TYPE B;
MEDLINE=98427137; PubMed=9746572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TremBtrel. 15, 01-OCT-2000 (TremBtrel. 15, 01-JUN-2001 (TremBtrel. 17, HEMOGLOBIN BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF221060; AAF80178.1; Interpro; IPR001993; Mitoch_carrier.Interpro; IPR000531; TonB_boxC.
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                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                               Haemophilus
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Infect. Immun. 68:4092-4101(2000).
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"Detection of Phase Variation in Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20316037; PubMed-10858226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-N182;
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TE; PS00215; MITOCH_CARTIER; UNKNOWN_1.
TE; PS01156; TONB_DEPENDENT_REC_2; 1.
NCE 993 AA; 113616 MW; A551BF3B2C64
PS00215; MITOCH_CARRIER; UNKNOWN_1 PS01156; TONB_DEPENDENT_REC_2; 1.
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Proteobacteria;
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8 (TrEMBLrel.
1 (TrEMBLrel.
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Lrel. 08,
Lrel. 17,
PROTEIN.
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15, Last sequence update)
17, Last annotation update)
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                                                                                                                                                                                                                                                                            gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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by Nontypeable
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Best Local
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01-MAY-2000 (TYEMBLEGI 1:
01-JUN-2001 (TYEMBLEGI 1:
01-JUN-2001 (TYEMBLEGI 1:
CG10042 PROTEIN.
CG10042 PR CG1793 1.
Drosophila melanogastor (1
                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VGA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cope L.D., Hrkal Z., Hansen E.J.;

**Dotaction of Phase variation in Expression of Proteins Involved Hemoglobin and Hemoglobin-Haptoglobin Binding by Nontypeable Haemophilus influenzae.;

**Infect. Immun. 68.4022-4101(2000).**

**EMBL: AF221059; AAF80176.1.**

**InterPro: IPR001993; Mitoch_carrier.

**InterPro: IPR001993; Mitoch_carrier.

**InterPro: IPR001993; TonB_boxC.**

**Tenerpro: IPR001993; TonB_boxC.**
         STRAIN-BERKELEY;
MEDLINB-2019606; PubMcd-10731132;
Adams M. D., Celniker S. E., Holt R. A., Evans C.A.
Ammanetides P.G., Scherer S. E., LI P.W., Hoskins
George R.A., Lewis S.E., Richards S., Ashburner
                                                                                                                                                                                                  Drosophila melanogastor (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00593; TonB_boxC; 1.
PROSITE: PS00215; MITOCH_CARRIER: UNKNOWN_1.
PROSITE: PS01165; TONB_DEPENDENT_RCC_2; 1.
SEQUENCE 1013 AA; 116260 MM; 769964335A4ED3C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KIV2;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KIV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20316037; PubMed-10858226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                           NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2;
Pred. No. 7.6e+02;
Mismatches 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1081 AA
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            Ashburner M., H
                                                   Evans C.A.,
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                                Gocayne J.D.,
A., Galle R.F.
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            Henderson S.N.
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SSEPPPRE
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RA BESCON K.Y., BENOS P.V., BERMAN D., BOLISHÄKOV S.R.
RA BOCKOVA D., BOCCHANN M.R., BOUCK J., BPOSKICIN P., BOCTHER P.,
RA BUTLIS K.C., BUSAND D.A., BUTLER H., CCATER A., CCHART I.,
RA CHERTY J.H., CAWLEY S., DANIKE C., DAVENDOTT L.B., DAVES P.,
RA CHERTY J.H., CAWLEY S., DANIKE C., DAVENDOTT L.B., DAVES P.,
RA CHERTY J.H., CAWLEY S., DANIKE C., DAVENDOTT L.B., DAVES P.,
RA DOGSON K., DOUP L.E., DOWNES M., DUGAN-ROCHA S., DUNCO B.C., DUNCO B.C.,
RA DOGSON K., DOUP L.E., DOWNES M., DUGAN-ROCHA S., PLOISON B.C.,
RA DOGSON K., DOUP L.E., DOWNES M., DUGAN-ROCHA S., PLOISON B.C.,
RA DOGSON K., DOUP L.E., DOWNES M., DUGAN-ROCHA S., PLOISON B.C.,
RA FOSIER C., GABYLEIS M. B., COFTEL J. J.H., CQ., FERTEZ G., FERTERS S., FLEISONMANN W.
RA FOSIER C., GABYLEIS M. B., ELGAMEN J.H., CG., CHARLEY M.H., LBEYSAM C.,
RA HARTIS N.L., HBYRYY D., HEIMAN T.J., HERNOND Z., KECHAM K.A.,
RA KIMMEL B. B., KOGITE C.D., KYAET C., KYNIZ Z., KRID D., LAI Z.,
RA KIMMEL B. B., KOGITE C.D., KYAET C., KYNIZ Z., KRID D., LAI Z.,
RA LASKO P., LAY Y., LAYYLISHY A.A., LI J., LI, MERSHOND J.M.,
RA MERKILOV G., MILSHIM N.V., MODARLY C., MORTIS J., MOSHNEFI N.,
RA MERKILOV G., MILSHIM N.V., MODARLY C., MORTIS J., MOSHNEFI N.,
RA MERKILOV G., MILSHIM N.V., MODARLY C., MORTIS J., MOSHNEFI N.,
RA MELSON D.R., PRISON K.A., HINDAY L., MURLDY D.M., YRLSON D.L.,
RA MELSON D.R., PRISON K.A., SINDREY N., PRICED J.M.,
RA MELSON D.R., PRICHOR C.S., PAN S., POLLAT J., PRICED J.M.,
RA SALVE S., STRADLING A.C., SCHAPLET C., KOPISH M.P., SMITH T.,
RA SPLET E., SPRADLING A.C., SCHAPLET C., MORD S., SIN B.,
RA SALVERSE N., WOODS T., SLAN M., STRONG R., SIN E.,
RA SYLTEKAS R., TRECTOR C., TURNER R., VENTER S., PAN S., TANO O., ENEMS L.,
RA KIMPL S. M., WOODS F. N., EDNOS Y., Show N., S., DAN M., S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA KIMPL S., MORD F. N., EDNOS Y., Show S., Zho O., Zheng L.,
RA KIMPL S., SHONG S., SHOP J., SHOP J., SONITH H.O.,
RA KIMPL S., SHOP S., SHOP J., SHOP J., SHOP J.,

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Best Local s
Matches 6
                                   Q9VHR2;
Q9VHR2;
Q1-MAY-2000
Q1-MAR-2001
Q1-MAR-2001
CG11729 PROT
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Fram: PP00288 PHD: 1.
Fram: PP00096 xf-c2H2: 1.
SMART: SM00349: PHD: 1.
SMART: SM00349: PHD: 1.
SMART: SM00349: PHD: 1.
SMART: SM00335: 7UDDR: 2.
SMART: SM00335: 7x C2H2: 1.
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InterPro; IPR001739; MBD.
InterPro; IPR001739; MBD.
InterPro; IPR001999; Tudor.
InterPro; IPR002999; Tudor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding;
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1. PROSITE: PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                     287
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                                   2001 (TrEMBLrel.
2001 (TrEMBLrel.
PROTEIN.
                                                                                                                                                                                                                                                                                                                                       Similarity
6; Conserv
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1081 AA; 119852 MW; D3417492763DD50B CRC64.
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                                                                                                 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                     292
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                           16,
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                                                           Last sequence update)
Last annotation update)
                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                       Score 30; DB 5;
Pred. No. 8.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 Length 1081;
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Drosophila melanogaster (Fruit fly)

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RESULT
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RA MAGNISH LO, Cellniker S.E., Hilp W., Hoskins R.A., Golle R.F.,

RA George R.A., Lewis S.E., Richards S., Sabburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutton R.C., Nogres Y. H.C., Blazej R.G., Chang O., Chen L.X.,

RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Change M., Pfeiffer B.D.,

RA Abril J.F., Agbyani A., An H.-J., Andrews Pfeinnkoch C., Ballevin D.,

RA Abril J.F., Agbyani A., An H.-J., Andrews Pfeinnkoch C., Ballevin D.,

RA Ballew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Drokstein P., Brottler P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler A.,

RA Bours R.C., Bussen D.A., Butter H., Cedieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Double B., Belcher A., Deng Z., Mays A.D., Dew I., Dletz S. M.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Helm H.H., Ibeyamn C.,

RA Kimmel B. B., Kodira C., D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Manil M., Kalush F., Karpen G.H., Kezutz S., Kulp D., Lai Z.,

RA Liu X., Mattel B., McIntosh T.C., McLood M., Kulpski M.P., McBson D.L.,

RA Liu X., Mattel B., McIntosh T., Lid J., Mintosh M., Nelson D.L.,

RA Manil M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local s
Matches (
                                                                  01-AUG-1998
01-AUG-1998
01-JUN-2001
STPK1
STPK1
Eukaryota; Euglenozoa; NCBI_TaxID=5664; [1]
                                                                                                                                                            060976;
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                                                 Leishmania major
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Pferryota; Neopiera; Endopieryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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nes 6; Conserv
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Gremblrel.
(Tremblrel.
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                                Kinetoplastida; Trypanosomatidae; Leishmania
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17,
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                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 1e+
); Mismatches
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01-NOV-1996
01-JUN-2001
1347 GSLGGS 1352
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Mol. Cell. Biol. 15:2754-2762(1995).
EMBL; U23146; AAA79517.1; -.
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-FISHER; TISSUE-EMBRYO;
MEDLINE-95257957; PubMed+7739556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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158 GSLGGS 16
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InterPro: IPP000709; Ser_th_Kln_actsite.
Pfam, PP00069; pkinase; 4
PF031TE: PS00101; PROTEIN_KINASE_DOW; 1
PROSITE: PS00108; PROTEIN_KINASE_ST| 1
ATP_blinding; Serine/throonine-protein_kinase; Transferase.
SEQUENCE 1557 AA; 16/902 MM; BC655561BBBD086A CRC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The nucleotide sequence of Leishmania major Friedlin chromosome 1.", Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARTY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AE001274. AAC24682.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yyırı r.u., Audleman L., Hixson G., Kiser P., Lemley C., Rickel E. Sisk E., Sunkin S., Swartzell S., Westlake T., Magness C., Bastien Pu G., Tvens A., Stuart K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelman I.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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STRAIN-FRIEDLIN;
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                                                                   1 GSLGGS 6
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                                                                                                                                            Similarity
6; Conserv
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1596 AA; 172498 MW;
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ilarity 100.
Conservative
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Pred. No. 1.7
0; Mismatches
                                                                                                                                       Score 30; DB 11;
Pred. No. 1.3e+03;
; Mismatches 0;
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RESULT Q9Z1F7

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Best Local
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                                                                                                                    Wotch (Amphibotch): evolutionary conservation of domains in amphicous and vertebrates." Submitted (APR-2000) to the EMBL/GenBank/DDBJ da EMBL, 12539; CAC19831.; ... InterPro; IPR002110; ANK. InterPro; IPR0021012; ARX_Dydroxyl. InterPro; IPR001012; ARX_Dydroxyl. InterPro; IPR0010152; ARX_Dydroxyl. InterPro; IPR0010418; EGF_01. InterPro; IPR0010418; EGF_01. InterPro; IPR0010418; EGF_01. InterPro; IPR0010418; EGF_01. InterPro; IPR0010400; Notch.
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Q9Z1F7;
Q9Z1F7;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2001
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SEQUENCE FROM N.A.
Chapline C., Mousseau B., Ramsay K.,
"Identification of a major protein ki
"Identification of a major protein ki
                    SMART;
                                        SMART;
                                                           PRINTS;
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01-MAY-1999 (TPEMBLEE) 17. Last sequence update)
01-UN-2001 (TREMBLEE) 17. Last annotation update)
PRC BINDING PROTFER AND SUBSTRATE
ROLLIS NOLVEGICUS (Rat). SUBSTRATE
BANKHYOTA: Metzoos. Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia; Bulkeria: Rodentia: Sciurognathi, Muridae; Murinae; Rattus.
                                                                                          Pfam;
                                                                                                             Pfam;
                                                                                                                                                                                                                                          Molland L.Z., Burgtorf C., Holland N.D., Lehrach H., Tamme R.,
Abl-Rached L., Pontarotti P., Lardelli M.
"Cloning and developmental expression of the amphioxus homologue of
                                                                                                                                                                                                                                                                                                                       Branchiostoma floridae (Florida lancelet) (Amphioxus)
Eukaryota: Metazoa: Chordata: Cephalochordata: Branch
                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
PUTATIVE NOTCH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 0:0-0(1995).
EMBL; U41453; AAD03788.1; -
INTERPO: IPRO01573; PKINALanch.
SEQUENCE 1596 AA: 172411 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformed cells.
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            SMART;
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                                                                                                                                                                                                                                                                                                                Branchiostoma
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                                                          ); PF00023; ank; 6.

); PF00008; EGF; 36.

); PF00066; notch; 3.

); PR00010; EGFBLOOU
MTS; PR00011; EGFLAMI
MTS; PR01452; NOTCH.
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                              SM00248;
SM00181;
SM00179;
                    SM00001;
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6; Conserv
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ilarity 100.0%;
Conservative (
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        9; ANK; 56.
1; EGF; 37.
1; EGF_CA; 34.
1; EGF_11ke; 13.
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0:0-0(1995).
                                                                     EGFBLOOD.
EGFLAMININ
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major protein kinase (
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17, Last
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Pred. No. 1.3
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Best Local S
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Q9C6G9;
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01-JUN-2001 (
01-JUN-2001 (
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PROSITE;
PROSITE;
EGF-11ke
SEQUENCE
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           STRAIN-CV. COLUMBIA.
                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2182 GSLGGS
                                      NCBI_TaxID=3702;
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PS500297; ANK_REPLROTION: 1.
PS00010; ASK_MYDROXYL: 1.
Ommin: Glycoprotein: Hydroxylation: Receptor. 5224 AA: 270959 MM; C2CA57E306D23EC9 CRC64:
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SEQUENCE FROM N.A.

MEDLINE-2117598: PubMed=11259647;

MIEDRINE-2117598: PubMed=11259647;

MIETRIAN H.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

POTOCKA I., MELSon W.C., Newton A., Stephens C., Phadke N.D., Ely

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

KOLONBY J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White

Salzberg S.L., Venter J.C., Shaptro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

TICES CROSST2; ANX22939.1;

TICES CROSST2.
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094943;
01-JUN-2001 (TrEMBLIFE1: 17, Created)
01-JUN-2001 (TREMBLIFE1: 17, Last sequence update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, Last amoctation update)
01-JUN-2001 (TREMBLIFE1: 17, CREMBLIFE)
01-JUN-2001 (TREMBLIFE1: 17, Last sequence update)
01-JUN-2001 (TREMBLIFE1: 17, CREMBLIFE)
01-JUN-2001 (TREMBLIFE1: 17, Last sequence update)
01-JUN-2001 (TREMBLIFE1: 17, Last sequence update)
01-JUN-2001 (TREMBLIFE1: 17, CREMBLIFE1: 17, Last sequence update)
01-JUN-2001 (TREMBLIFE1: 17, Last sequence update)
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; akagnollophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                              (TrEMBLrel. 17, Created)
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E TRANSPOSASE, PUTATIVE.
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Pred. No. 1.4e
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                                               Embryophyta; Tracheo 
edons; core eudicots;
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RA MHOLOGIS A. BCKET J.R., Palm C.J., Fedderspiel N.A., Kaul S.,
RA WHITE O. Alons J. Altafi H. Araujo R., Bowman C.L., Brooks S.Y.,
RA WHITE O., Alons J. Altafi H. Araujo R., Bowman C.L., Brooks S.Y.,
RA Glandy M. K., Conn L., Altafi H., Araujo R., Chesk R.F., Chin C.W.,
RA Chang M. K., Conn L., Chao Q., Chen H., Check R.F., Chin C.W.,
RA Glid J.E., Goldsmith A.D., Hasas B., Hansen N.F., Hughes B., Hujfar L.,
RA Hunter J.L., Jenkins J., Johnson-Ropson C., Khan S., Khayin E.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Millischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Millischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
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RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
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RA Will J., Vu G., Fraser C.M., Venter J.C., Davis R.M.,
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Submitted (MAR-2000) to the
EMBL; AL162873; CAB85515.1;
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Bevan M., Peters S.A., v.
Bancroft I., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-CCT-2000 (TrEMBLrel. 15, Cre
01-CCT-2000 (TrEMBLrel. 15, Las
01-CCT-2000 (TrEMBLrel. 15, Las
HYPOTHETICAL 28.4 KDA PROTEIN.
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EMBL; AC079287; AAG50848.1;
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Pred.
1; Mis
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Pred. No. 3.96
1; Mismatches
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OSFL20 PRELLARANCE
OSFL20 PRELLARANCE
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OI-MAR 2001 (TrEMBLrel. 16, Last sequence update)
OI-MAR 2001 (TrEMBLrel. 16, Last annotation update)
OI-MAR 2001 (TrEMBLrel. 16, Last annotation update)
OI-MAR 2001 (TREMBLREL 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q53815; PRELIMINARY;
Q53815;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
                                                                                                                                                                                                                                                                                                                     EMBL; X78972;
NON_TER 26
SEQUENCE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces bluensis.

Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria: Firmicutes; Atroptomycineae; Streptomycetaceae; St
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Submitted (APR-1994) to the I
EMBL; X78972; CAA55568.1; -.
NON_TER 267 267
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
HYPOTHETICAL PROTEIN TA0226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of the acidophilum."; Nature 407:508-513(2000). EMBL; AL445063; CAC11371.1;
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Ruepp A., Graml W., Santos-Martinez M.-L.,
Mewes H.-W., Frishman D., Stocker S., Lupar
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Archaea; Euryarchaeota; 1
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1; Mismatches
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Pred. No. 4.1e+02;
1; Mismatches (
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3.9e+02;
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01-MAY-2000
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Ephydroidea; Drosophi
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudioctyledons; core eudicots; kosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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) (TrEMBLrel. 13,
) (TrEMBLrel. 13,
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83
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ilidae; Drosophila.
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RA Admis H.D., Celniter S.E., Lil P.W., Hoskins R.A., Gocayne J.D.,
RA Admis H.D., Celniter S.E., Richards S. Ashburner M., Henderson S.N.,
RA Admis H.D., Celniter S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chene I.X.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chene I.X.,
R. Stutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chene S.N.,
RA Stutton R.C., Rogers Y.-H.C., Elazel R.G., Champe M., Pfeiffer B.D.,
RA Stutton R.C., Rogers Y.-H.C., Elazel R.G., Champe M., Pfeiffer B.D.,
RA Hanley R.M., Basu A., Baxter E.G., Helt G., Malson C.R., Hiklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfeinnkoch C., Baldvin D.,
RA Ballew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.M.,
RA Ballew R.M., Basu A., Barenan B.P., Bhandari D., Bolshakov S.M.,
RA Barley E.M., Basu A., Baller H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Bolchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Bolchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Bolchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise R.,
RA Cherry J.M., Cawley S., Dahlke C., Borcha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Borrice S., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze C., Fertze
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Science 287:2185-2195(2000).
ElyBase: Pegn003943; C05468.
ElyBase: Pegn003943; C05468.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etwaryota; Medazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-NOV-1998 (TERMELTel. 08, Last sequence update)
01-JUN-2001 (TERMELTEL. 17, Last annotation update)
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang
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CG4585 OR ANON-60AB.
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Adams N.D., Cenlher S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Mannatides P.G., Scherer S.E., Lif P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Stutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., RA Sutton R.C., Rogers Y.-H.C., Blazes P.G., Champe M., Pesiffer B.D., Ray Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ray Man R.H., Dank P.W., Berman B.P., Bardward D., Belshako P.G., Balawin D., Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M., Ray Beeson K.Y. Beans P.V., Berman B.P., Bhandari D., Belshakov S., Ray Borkova D., Betchan M.R., Bouck J., Brokretin P., Brottier A., Chandra I., Ray B. C., Burtis K.C., Busam D.A., Butler H., Caddou E. C., Brottier A., Dankov B.C., Davenport L.B., Davies P.R., Bordson K., Doup L.E., Downes M., Dugan-Rocha S., Dietz S.M., Podson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W., Ray B.D., L., Larres K., Ray Borts R., Gelbart M.M., Glasser K., Ray Godek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M., Flasser K., Ray Godek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hannel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Bukaryota; Metazoa; Arthropoda; Trachaeta; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BMBL; AB003462; APR47081.1; -

EMBL; AB010264; BAA3269.1; -

EMBL; AB010261; BAA3269.1; -

E1yBase; FBp0002335; CQ4586;

InterPro; IPR000462; CDP-OH_P_transf.
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Wang Z.-Y., W
Williams S.M.
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MEDLINE-9208659; PubMed-10191082;
LUKecsovich T., Asztalos Z., Juni N., Awano W., Yamamoto D.;
"The Drosophila melanogaster 50A chromosomal division is extremely dense with functional genes: their sequences, genomic organization, and expression.;
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Pred. No. 6.5e+02;
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X., Smith H.O.,
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RA Lili X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G.,
RA Ralazzolo M., Fittman G.S., Pan S., Pollard J., Puri Y., Reese M.G.,
RA Palazzolo M., Siden K.A., Nixon K., Nusskern D.R., Scheler F., Shen H.,
RA Shue B.C., Siden K.Amouders R.D.C., Scheler F., Shen H.,
RA Shue B.C., Sirdelin A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Stradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syliraks R., Toctor C. Turner R., Venter E., Wang A.H., Wang X.,
RA Syliraks R., Toctor C. Turner R., Venter E., Wang A.H., Wang X.,
RA Syliraks R., Toctor C. Turner R., Venter E., Wang S., Yao O.A.,
RA Yilliams S.M., McOdage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Yilliams S.M., McOdage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Yilliams S.M., Worley R., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Yilliams S.R., Zhou S., Rubin G.M., Venter J.C.,
RA Yilliams S.R., Wyers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosphila melanogaster.*;
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DR ENBL, MR003398, A7008 M. 7660 A710 A810 TROSPANCIATRAGED COLL.
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Matches 5; Conserv
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                                                                                                      Beekvilder M.J., Nieuwenhuizen R., van Duin J.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
EMBL: AEU5925; AACI45891.; -
SEQUENCE 421 AA; 48486 MM; 3978CB9E7E9D0943 CRC64;
                                                                                                                                                                                                        MEDILINE-96190948; PubMed-8609616;
Becketldor J., Nieuwenbuieen R., Poot R., van Duin J.;
"Secondary structure model for the first three domains
Control of A-procein synthesis.";
J., Mol. Biol. 256:8-19(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, serogroup III. NCBI_TaxID=75723;
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01-NOV-1998
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Pred. No. 6.8e+02;
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MAILLY J.F., Mybdynik A., Ali H.-U., Aluckwys-Frankoch L., Beaslay E.M.,

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Ra Bockon K.D., Bende J.P., Bhandani D., Bolishkov S.C., Brother C.,

Ra Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davdes P.,

Ra Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davdes P.,

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Amannetides PG. Scherer S.E., IL PM. Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Asbburner M., Henderon S.N.,
Sutton G.G., Woortnan J.R., Yandell M.D., Zhang Q., Chan L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer, B.D.,
Mon K.H., Doyle C., Baxter E.G., Helt G., Neason C.R., Mikios G.L.G.,
bbill J.F., Agbayani A., An H., J., Anddews-Ffannoch C., Beidduin D.,
bbill J.F., Agbayani R.A., An H., J., Anddews-Ffannoch C., Beidduin D.,
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MEDLINE=20196006; PubMed=10731132;
Anisker S.E., Holt R.A.,
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Tnsecta;
Pterygota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                          DNA-binding; Developmental protein; Nuclear protein; Paired
                                                                    PROSITE; PS00034; PAIRED_BOX; 1
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Q07426;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-2001
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Ekkaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinide; Cyprinine; Carassius.
(KSI_TaxLD-7937;
                                                                                                                 J. Comp. Neurol. 340:269-280(1994).
EMBL; L09743; AAC38008.1; F.
INTERPRO; IPRO01664; IF.
INTERPRO; IPRO02957; KERRÍLI.
PÉAM, PF00183; Éllament; 1.
PRINTS; PRO1248; TYPELKERATIN.
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MEDLINE-94259853; PubMed-7515399;
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1; Mismatches 0;

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                                                         Score 28; DB 13; Length 455; Pred. No. 7.7e+02;
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Sequence 61, Appl
Sequence 61,
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**US-08-828-712-11** 

Sequence 11,

GENERAL INFORMATION:

NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: TITLE OF INVENTION:

ADDRESSEE:

STREET: 1001 G STATE: Washington

COMPUTER READABLE FORM:

ZIP: 20001 COUNTRY:

U.S.A.

## ; INDIVIDUAL ISOLATE: Ig kappa peptide linker US-08-828-712-11 Sequence 11, Application US/09063276 Patent No. 6140113 GENERAL INFORMATION: APPLICANT: Schneck, Jonathan APPLICANT: O'Herrin, Sean APPLICANT: O'HERRIN, Sean TITLE OF INVENTION: Molecular Complexes Which TITLE OF INVENTION: Modify Immune Responses NUMBER OF SEQUENCES: 20 ATTORNEY/AGENT INFORMATION: NAME: Kagan, Sarth A. REGISTRATION NUMBER: 32,141 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICANT: Schneck, Jonathan P. APPLICANT: O'Herrin, Sean MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: US/08/828,712 FILING DATE: 28-MAR-1997 1, Application US/08828712 6015884 1001 G Street, N.W. Banner & Witcoff, Ltd Banner & Witcoff Soluble Divalent and Multivalent Heterodimeric Analogs of Proteins 01107.73713 0 Score 30; DB 3; Pred. No. 1.6e+05; ALIGNMENTS Mismatches Length 6; Indels .0 Gaps 0; US-08-635-121-2 ; Sequence 2, Application US/08635121 ; Patent No. 5910442 밁 ş US-09-063-276-11 RESULT Query Match 100.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0 APPLICATION NUMBER: 08/988/7 FILING DATE: 28-MAR-1997 APPLICATION NUMBER: 60/014,3 FILING DATE: 28-MAR-1996 ATTORNET/ACENT INFORMATION: NAME: Kagan, Sarah A REDISFRATION NUMBER: 32141 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette CLASSIFICATION: 514 PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: APPLICANT: Gelman, Irwin H. TITLE OF INVENTION: TUMOR SUPPRESSOR GENE PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS FILING DATE: ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: STREET: 1001 G St CITY: Washington CLASSIFICATION: OPERATING SYSTEM: SOFTWARE: FastSEC COMPUTER: CITY: New York TYPE: amino acid STRANDEDNESS: sir TELEPHONE: 202-508-91 TELEFAX: 202-508-9299 APPLICATION NUMBER: FILING DATE: 21-AF SOFTWARE: FastSEQ for Windows Version 2.0 OPERATING SYSTEM: COUNTRY: APPLICATION NUMBER: US/08/ FILING DATE: 19-APRIL-1996 ZIP: COUNTRY: STATE: STREET: TOPOLOGY: linear LENGTH: APPLICATION NUMBER: ADDRESSEE: 1 GSLGGS 6 1 GSLGGS 6 20001 10112-0228 8 NY 30 Rockefeller Plaza 6 amino acids 1001 G Street, USA USA IBM Compatible IBM Compatible Brumbaugh, Diskette UMBER: 08/828,712 28-MAR-1997 21-APR-1998 single 60/014,367 US/09/063,276 US/08/635,121 Graves, 0 01107.74154 Score 30; DB 4; Pred. No. 1.6e+05; Mismatches Donohue & Raymond Length 6; Indels 0 Gaps 0;

TELEFAX: (202)508-9299
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

TELEPHONE:

(202)508-9100

CLASSIFICATION: 514

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Matches Query Match

Local Similarity hes 6; Conserv

Conservative

100.0%;

1 GSLGGS 6 GSLGGS 6

FRAGMENT TYPE: ORIGINAL SOURCE:

internal peptide

MOLECULE TYPE: PO

TOPOLOGY: linear TYPE: amino acid

STRANDEDNESS LENGTH: 6 amino acids

us-09-063-276-11

COPRESPONDENCE ADDRESS: NADDRESSEE:

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: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
US-08-635-121-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45, Application US/08014153D
GENERAL INFORMATION:
APPLICANT: Hadlock, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                  TELEPHONE: (415) 369-9500
TELEPAX: (415) 369-9500
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CLARK, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: A300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEPAX: 212-765-2519
                                                                                                                                                                           APPLICATION NUMBER: US/08/014,153D FILING DATE: 05-Feb-1999 FILING DATE: 05-Feb-1999 FRIOR APPLICATION DATA: CORROSSISTATION DATA: APPLICATION UNBER: US 07/653,091 APPLICATION WHERE: US 07/653,091 APPLICATION WHERE: US 07/366,313 APPLICATION WHERE: US 07/6548,270 FILING DATE: 31-DEC-1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960 GSLGGS 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A.
REGISTRATION NUMBER: 36,373
                                                                                        REFERENCE/DOCKET NUMBER: G4C1P3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penabscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method and Assay for HTLV NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Redwood City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goh, Chin-Joo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coung, Steven K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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RESULT 6
US-09-041-991A-10
              ; Sequence 10, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 39,355
REFERRING/DOCKET NUMBER: NA-7
REFERRING/DOCKET NUMBER: NA-7
RELEPHAN: (352) 372-5800
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-014-153D-45
                                                                                                                                                                                Matches
                                                                                                                                                                                              Best Local
                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                    349 GSIGGS 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                  1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/041,991A FILING DATE: 13-MAR-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2421 N.W.
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GSMGGS 15
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                                                                                                                                                                           93.3%;
Similarity 83.3%;
5; Conservation
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                                                                                                                                                                                                                                                                                                                         633 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                        Score 28;
Pred. No. 5
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Pred. No.
                                                                                                                                                                             Mismatches
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Mismatches
                                                                                                                                                                       7e+02;
0;
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APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: TOXIS Active Against Pests
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

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Query Match
Best Local Similarity
Matches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-704-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08704931
Patent No. 5885797
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE,DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 24-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOTTWARE: PATENTIAL
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             APPLICANT: Chen, Chao-Min (Amy)
APPLICANT: Groudino, Mark
APPLICANT: Groudino, Mark
APPLICANT: Groudino, Mark
APPLICANT: Molinical Marchd
APPLICANT: Molinical Moleculer Moleculer
TITLE DE INVENTION: INC. 5885797e1 DNA Sequences Encoding Proteins
TITLE DE INVENTION: INCOVER IN MOSCENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
# APPLICATION NUMBER: US/08/704,931
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 GSIGGS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/041,991A FILING DATE: 13-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                     STREET: 1218 r
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                             ADDRESSEE: Stratton Ballew, STREET: 1218 Third Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSLGGS 6
FILING DATE:
                                                                                                                                                     98101
                                                                                                                                                                                          W
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%;
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 3; Le Pred. No. 5.7e+02; 1; Mismatches 0;
                                                                                                                                                                                                                               Suite 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Best Local Similarity Matches 5; Conserv Query Match

Conservative

90.0%;

Score 27; DB 2; pred. No. 3.3e+02; 1; Mismatches

DB 2;

Length 246;

Indels

0

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, MOLECULE TYPE: protein US-08-704-931-6
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; MOLECULE TYPE: protein US-08-704-931-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08704931 Patent No. 5885797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-682-0446
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Chen,
                                                                                                                               CLASSIPTION: 536
ATTORNEY AGENT INFORMATION:
NAME: YAGENT INFORMATION:
REJERNATION NUMBER: 38,515
REJERNATION NUMBER: 38,515
TELEPHONE: 206,685-1196
TELEPHONE: 206,685-1196
                                                                                                   TELEFAX: 206-682-0446
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: HUTELECOMMUNICATION INFORMATION: 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: King, Jeffrey J
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 5885797el DNA Sequences Encoding Proteins TITLE OF INVENTION: Involved in Myogenesis NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                  TYPE: amino acids
TOPOLOGY: liper:
WOLECHIEF
                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,931
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Groudine, Mark
APPLICANT: Weintraub, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kraut, No. APPLICANT: Groudine, 1
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GALGGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 200-0-0446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1218 T
CITY: Seattle
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Stratton Ballew, PLLC STREET: 1218 Third Avenue, Suite 1313
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                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                      206-682-0446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, Chao-Min (Amy)
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Pred. No. 2.1e+02;
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GSLGGS 6

US-08-704-931-4 RESULT 9 US-08-704-931-4 멍 Sequence 4, Application US/08704931 Patent No. 5885797 TELEPHONE: 206-683-1496 TELEFAX: 206-682-0446 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION:
NAME: King, Jeffrey J
REGISTRATION NUMBER: 33,515
REFERENCE/DOCKET NUMBER: HU11
TELECOMMUNICATION : TELEPHONE: 206-683-1496 GENERAL INFORMATION: TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: TITLE OF INVENTION: APPLICANT: Groudine, Mark
APPLICANT: Weintraub, Harold APPLICANT: 120 GALGGS 125 STREET: 1218 TO CITY: Seattle STATE: WA NUMBER OF SEQUENCES: 120 GALGGS 125 LENGTH: CLASSIFICATION: APPLICATION NUMBER: US/08/704,931 FILING DATE: COUNTRY: ADDRESSEE: Stratton Ballew, PLLC STREET: 1218 Third Avenue, Suite 1313 1 GSLGGS 6 98101 251 amino acids ASU Chen, Chao Min (Amy) Kraut, No. 5885797bert Kraut, No. 5889 Groudine, Mark 536 No. 5885797el DNA Sequences Encoding Proteins Involved in Myogenesis 23

HU11.PO2

В Query Match
Best Local Similarity |
Watches 5; Conservat Conservative 90.0%; Score 27; Pred. No. Mismatches 3.4e+02; DB 2; Length 251; Indels 0

Gaps

0;

US-09-237-543-4 GENERAL INFORMATION:
APPLICANT: KARPELIET, ROSENA
TITLE OF INVENTION: MOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: MOUSE MAD USES THEREOF
FILE REFERENCE: 035800/13531
CURRENT PELLOATION WHERE: US909/237.543A
NUMBER OF SEQ ID MOS: 19-01-26
SOPTMARE: Patentin Ver. 2.0 Sequence 4, Application US/09237543A Patent No. 6143540

RESULT 12 US-09-237-543-2

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309 GSVGGS 314

1 GSLGGS 6

Best Local Similarity Matches 5; Conserv. Query Match

Conservative

90.0%;

; Score 27; DB ; Pred. No. 4.3e 1; Mismatches

DB 2; 3e+02

Length 318;

Indels

0

0

peptide

TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: pepti US-08-633-148-4 ĝ OTHER INFORMATION. Description of Artificial Sequence: eukaryotic OTHER INFORMATION: protein kinase domain US-09-237-543-4 Sequence 4, Application US/08633148 Patent No. 5864018 Query Match 90.0 Best Local Similarity 83.2 Matches 5; Conservative TELEPHONE: (415) 326-2400 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 4: GENERAL INFORMATION:
APPLICANT: MORSER, MICHAEL REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGETT INFORMATION:
NAME: MURRHY ESQ., MATTHEN B. ORGANISM: Artificial Sequence FEATURE: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TYPE: PRT SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND TITLE OF INVENTIONS. LENGTH: 254 NUMBER OF SEQUENCES: APPLICANT: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: U.S.A. REGISTRATION NUMBER: ENGTH: 41 GSLGGA 46 1 GSLGGS 6 318 amino acids NAGASHIMA, MARIKO HOLLANDER, DORIS A. PatentIn Release #1.0, Version #1.30 single 90.0%; US/08/633,148 39,787 014618-005600US Score 27; DB 4; Pred. No. 3.4e+02; Mismatches RECEPTOR POLYPEPTIDES AND USES THEREFOR Length 254 Indels 0 Gaps

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US-09-237-543-2
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US-08-633-148-2
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Best Local S
Matches 5
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APPLICANT: KARPALIEY, ROSANA
APPLICANT: KARPALIEY, ROSANA
TITLE OP INFUNITON: NOVEL MOLECULES OF THE HXID-1-RELATED PROTEIN PAMILY
TITLE OP INFUNITON: AND USES THEREOF
FILE REFERENCE: 0.35800/175631
CURRENT APPLICATION WHERER: US/09/237.543A
CURRENT APPLICATION WHERER: US/09/237.543A
CURRENT FILING DATE: 199-01-26
NUMBER OF 560 ID NOS: 191-01-26
SOPTMARE: PRICHILIN Ver. 2.0
SOPTMARE: PRICHILIN Ver. 2.0
SOUTHARE: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA
                                                                              TYPE:
                                                         STRANDEDNESS:
                                                                                                 LENGTH:
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                     peptide
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Pred. No. 4.4e+02
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Fest Local Similarity

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Score 27; Pred. No.

DB 2; 4.6e+02;

Length 340

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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-630-172-6
                                                                                                                                                                                                                                   US-09-375-419-6
                                                                                                                                                                                               ; Sequence 6, Application US/09375419 ; Patent No. 6264950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08630172
Patent No. 6060054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 863-970
TELEPAX: (303) 863-0223
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                               GENERAL INFORMATION: UWC APPLICANT: Staerz, UWC APPLICANT: STAERZ, UWC TITLE OF INVENTION: LYMPHOCYTE VETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TIRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-COS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OFFICIATION NUMBER: US/08/630,172
FILICATION NUMBER: US/08/630,172
FILICATION NUMBER: US/08/630,172
FILICATION NUMBER: US/08/630,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T TITLE OF INVENTION: LYMPHOCYTE VETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Staerz,
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                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     156 GSLGGT 161
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CITY: I
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                            STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
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              COUNTRY:
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                                                                                ADDRESSEE:
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pred. No. 4.7e+02;
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

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                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-COMPACIBLE SOPTIANCE PATENTING SYSTEM: PC-COSC/MS-T-OS SOPTIANCE PATENTING PATENTING DATA:

APPLICATION NUMBER: US/08/464 >cc
PILING DATE: US/08/464 >cc
CLASSIPET: US/08/464 >cc
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 6:
                                                                                           FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 04-FEB-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ORO, Ph.D., ANTHONY E.
APPLICANT: EVANS, Ph.D., RONALD M.
TITLE OF INVENTION: INSECT RETUNCTD-LIKE RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER: P41 9966
                                        NAME: Reiter,, Stephen E. REGISTRATION NUMBER: 31,1
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/375,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JE: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 amino acids
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                                                                                                                                                                                 US 07/497,935
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Pred. No.
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Query Match
Best Local Similarity
Matches 5; Conserve
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US-08-464-266-2
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Best Local Similarity 83.3
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                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,975
FILING DATE: 04-FEB-1993
APPLICATION NUMBER: US 07/497,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DBO, Ph.D., ANTHONY E.
APPLICANT: EVANS, Ph.D., RONALD M.
TITLE OF INVENTION: INSECT RETINOID-LIKE RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEGUENCES: 5
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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LENGTH: 513 amino acid
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                                                                                                                       TYPE: amin
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                                                                                                                                                                                                                                                NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      LENGTH:
                                                                                                                                                                                                  TELEPHONE: 619-546-47
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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amino acid
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                          Score 27; DB 1;
Pred. No. 7.1e+02;
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Pred. No.
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                                         Length 513;
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Best Local Similarity
S; Conserve
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                                                                                                                      Sequence 2, Application US/08486403 Patent No. 6281330
                                                                                      GENERAL INFORMATION:
APPLICANT: EVANS, RONALD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 546-93
                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release 11.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,514 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SECHAVES, WILLIAM A.
APPLICANT: YAO, TSO-PANG
TITLE OF INVENTION: MULTIMERIC FORMS OF MEI
TITLE OF INVENTION: STEROID/THYROID SUPERFO
TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCKEOWN, MICHAEL B. APPLICANT: ORO, ANTHONY E.
                                                                                                                                                                                                                             200 GSVGGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARF: Detects Delega #1 0
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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    INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                ORO, ANTHONY E.
SEGRAVES, WILLIAM A.
YAO, TSO-PANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619)
                                                                   MCKEOWN, MICHAEL B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (619) 546-4737
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  MULTIMERIC FORMS OF MEMBERS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07/907,908
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Pred. No. 7.
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-403-2
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                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5959
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Matches 5; Conservative
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APPLICATION NUMBER: US 07/907,

APPLICATION NUMBER: US 07/907,

PILLING DATE: 02-JUL-192

ATTORREY, AGENT LAFORMATION:

NAME: REGISTRATION NUMBER: 93192

REFERENCE/DOCKET NUMBER: 941 9,

TELECOMMUNICATION INFORMATION:

TELECHONE: (619) 546-4377

TELECHONE: (619) 546-3932
                                                                                                                                                                                                                                                                          APPLICANT: Hein, Mich B.
APPLICANT: Hiatt, Andrew C.
APPLICANT: Ma, Julian K.C.
TITLE OF INVENTION: TRANSCENIC I
TITLE OF INVENTION: SECRETORY AND AND ADDRESS OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
             COMPUTER READABLE FORM:

MEDIUM TYPES Floppy disk
COMPUTER: IBM PC COMPUTED BE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-TOS/MS-DOS
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 444
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 GSVGGS 205
                                                                                                                                                                            STREET: 10666 NO.
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                               COUNTRY: U
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
FILING DATE:
                                                                                                                                                                                                                      ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE STREET: 1066 No. 5959177th Torrey Pines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9007
                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08642406A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PRETTY, SCHROEDER, BRUEGGEMANN & 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                    S
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03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE ULTRASPIRACLE RECEPTOR
                                                                                                                                                                                                                                                                                                  TRANSGENIC PLANTS EXPRESSING ASSEMBLED SECRETORY ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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tches 0;
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                                                                                                                                                                                                                           Road, TPC-8
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 02-OCT-1990
PRIOR APPLICATION DATA:

US 07/591,823

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RESULT 21
US-08-434-000A-2
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TELECOMBUTCATION INCOMATION:
TELEPRONE: (619) 554-2937
TELEPRONE: (619) 554-6312
INCOMATION FOR SPO ID NO 122:
SEQUENCE CHARACTERISTICS:
LEWSTH: (24 aniso acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08434000A Patent No. 6046037
                                PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including ap
PRIOR APPLICATION DATA: described be
APPLICATION NUMBER: 08/367,395

PRILING DATE: 13/30/94

APPORNEY/ACREM INFORMATION:
REGISTRATON NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:
PELEPHONE: 6(13) 552-80

THIEFENA (6(13) 552-80

THIEFENA (6(13) 552-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yuery match 90.0%;
Best Local Similarity 83.3%;
Matches 5. Common 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
APPLICANT: K.-C. TOMAS LEHNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 53 West Fith Street
STREET: 53 West Fith Street
STREET: Suite 4700
CITY: Los Angeles
STRIE: Californ.
                                                                                                                                                                                                                                                              SOPTWARE: WOR'D PETFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE:
CLASSTOTATION
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/427,765 FILING DATE: 27-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 GNLGGS 255
TELEPHONE: (619) 552-84
TELEFAX: (619) 552-0159
TELEX: 67-3510
                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        90071
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                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULINS CONTAINING PROTECTION
                                                                                                                                                                         : including application
: described below:
08/367,395
                                                                                                                                                                                                                                                                                            US/08/434,000A
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Pred. No. 8.7e+02;
                                                                                                                                                                                                                                                                                                                                                     DOS 5.0
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; SEQUENCE DESCRIPTION: Rabbit polyimmunoglobulin receptor US-09-312-157-2
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US-09-312-157-2
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Best Local Similarity
Watches 5; Conserve
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Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: SEQUENCE LISTING INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 GNLGGS 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                              NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,6:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/434,000 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANY: ANDREW C. HIATT, JULIAN
TITLE OF INVENTION: IMMUNOSIOBULINS CONTAINING PROTECTION
                                                                                                                                                                                TELEFAX: (619) 552-0159
TELEX: 67-351
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/312,157 FILING DATE: 14-May-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                    ropology: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90073
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                                                                                                                                                            SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: IBM P.C. DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        storage
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Pred. No. 1.1e+03;
""cmatches 0;
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Query Match Best Local Similarity

90.0%;

Score 27; DB 4; Length 773; Pred. No. 1.1e+03;

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US-08-867-941-13
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                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                 Sequence 13, Application US/08867941 Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE/DOCKET NUMBER: 29938-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 404-7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Klein, Michel H
TiTLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSE, TIMOTHI APPLICANT: BOSCH, MARNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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APPLICANT: TODARO, GEORGE J.
                                                                                                                APPLICANT:
                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 GNLGGS 255
                                                                                                                                                                                                                                                                                                                                                                    133 GSLGGN 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MOKKLOUM FAREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSLGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GSLGGS-6
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                                                                                                                Du, Run-Pan
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linear
                                                  Wang, Quijun
Yang, Yan-Ping
                                                                                                                                           Loosmore, Sheena M
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Pred. No. 1.4e+03;
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Best Local Similarity
Matches 5; Conservi
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPATIBLE OF COMPA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
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COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Relace
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ZIP: M5G 1R7
                                                                                 APPLICATION NUMBER: US/08/867,941 FILING DATE: 03-JUN-1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
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CITY: Toronto
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TYPE: amino acid
   REGISTRATION NUMBER: 24,973
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M5G 1R7
                               Stewart,
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Du, Run-Pan
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                               Michae.
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Pred. No. 1.4e+03;
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Length 985 Indels

0; Gaps

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SOTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/867,941 FILING DATE: 03-JUN-1997
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1038-681 MIS: jb
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us-09-074-658-13
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                                                              Matches
                                                                                         Query Match
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ENFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (410) 595-1155
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: U8/09/074,658
FILING DATE: 08-MAY-198
CLASSIFICATION: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Stewart, michael I
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APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
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175 GALGGS 180
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APPLICANT: Klein, Michel H
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                                                            Local Similarity
les 5; Conserv
                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                        LENGTH:
                            1 GSLGGS 6
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nes 5; Conserv
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STRANDEDNESS: sir
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                                                                                                                                                                                               985 amino acids
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6th Floor, 330 University Avenue
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                                                            Conservative
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                                                                                                                                                       linear
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                                                     Score 27; DB 4;
Pred. No. 1.4e+03;
1; Mismatches (
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                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                           Sequence 12, Application US/08867941 Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3%;
Matches 5; Conservation
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCTWARE: PAtentin Release #1.0, Version #1.30
SUSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-199
ATTORNEY/AGENT INFORMATION:
AMBE: STREET INFORMATION:
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                                                                                                 APPLICANT: LOOSMOTE, Shcena
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFER
                                                                                                                                                                                                        GENERAL INFORMATION:
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                                           ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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            ADDRESSEE: 54...
ADDRESSEE: 54...
                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               175 GALGGS 180
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APPLICANT: Klein, Michel
TITLE OF INVENTION: LACTO
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TELEFAX: (416) 595-1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M5G 1R7
Ontario
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Quijun Wang
                                                                                                                                                                                       Loosmore, Sheena M
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h Floor, 330 University Avenue
                                                                                               LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595-1155
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                             330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheena M
                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Pred. No. 1.4e+03;
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US-08-867-941-16
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CLASSICATION: 03-JUN-199
CLASSICATION: 0435
ATTORNEY/AGENT INFORMATION:
NAME: SECWART, NICHAEL I:
REGISTRATION NUMBER: 24.973
REFERENCE/DOCKET MUMBER: 1038-681 M:
REFERENCE/DOCKET MUMBER: 1038-681 M:
TELEFORME : 0416, 959-1163
INCOMMITION: 0416, 959-1163
INCOMMITION FOR SED ID MO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08867941 Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                     TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible operating SYSTEM: PC-00S/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                          NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPETIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOOSMOTE, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Kein, Michel H
TITLE OP INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELIA
                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                    SECVENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 83.
                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                             ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
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R READABLE FORM:
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6th Floor, 330 University Avenue
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1000 amino acids
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Pred. No. 1.4e+03;
1; Mismatches 0;
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; TYPE: amino acid
; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-867-941-16
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                                              RESULT 31
US-09-074-658-16
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Best Local Similarity
S; Conserve
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; Sequence 16, Application US/09074658 ; Patent No. 6184371 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09074658 Patent No. 6184371
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LOOSMOTE, Sheer APPLICANT: Run-Pan Du APPLICANT: Quijun Wang APPLICANT: Yang, Yan-Ping APPLICANT: Kiein, Michel i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,658
                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,97:
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                              190 GALGGS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
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CITY: Toronto
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                          1 GSLGGS 6
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                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                          linear
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Pred. No. 1.4e+03;
                                                                                                                                                                           Score 27; DB 4; L4
Pred. No. 1.4e+03;
1; Mismatches 0;
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US-08-484-438-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                  NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                  APPLICANT: Helistr m, Ingegerd
APPLICANT: Helistr m, Karl E.
TITLE OF INVENTION: HERA HUMAN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                          APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 595-1155
                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       COUNTRY: U.S.A.
                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 08-MAY-1998 CLASSIFICATION: 435
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                                                                         10036-2711
                                                                                                      New York
                                                                                                                                     1155 Avenue of the Americas
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6th Floor, 330 University Avenue
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Pred. No. 1.4e+03;
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US-09-074-658-15
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; MOLECULE TYPE: protein
US-08-484-438-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6184371
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09074658 Patent No. 6184371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 24 NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: I
APPLICANT: I
                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NAVA:
APPLICATION NUMBER: US/09/074,658 EILING DATE: 08-MAY-1998 CLASSIFICATION: 435
                         ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael T
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1060 GNLGGS 1065
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REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yang, Ya
APPLICANT: Klein, M
TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: 14-OCT-
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            ZIP: M5G 1R7
                                                                                                                                                                                                                                                           STATE: Ontario
                                                                                                                                                                                                                                                                                  STREET: 6th F1
CITY: Toronto
                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                          Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 Run-Pan Du
Quijun Wang
                                                                                                                                                                                                                                                                                                                                                                                                            Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loosmore, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMBER: US 07/981,165
24-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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Pred. No. 1.9e+03;
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US-09-074-658-11
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US-09-074-658-15
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Best Local Similarity 83.0
Matches 5; Conservative
                                                                  Matches
                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
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  1668 GALGGS 1093
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
AND TOATTON TOAT SEC
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LENGTH: 2432 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2439 amino ac1
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMOTE, Sheer APPLICANT: Run-Pan Du APPLICANT: Quijun Wang APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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CITY: Toronto
STATE: Ontario
                                                                Local Similarity
hes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1038-795
                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                1 GSLGGS 6
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                                                                                                                                                                                                                2439 amino acids
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                                                                    Conservative
                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sim & McBurney
                                                                                                                                                                                                                                                                                   (416) 595-1155
                                                                                                                                                                              single
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                                                                                  90.0%;
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                                                                Score 27; DB 4; LL
Pred. No. 3.6e+03;
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Pred. No. 3.6e+03;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-609-716-16
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US-07-609-716-16
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US-07-609-716-67
                                                                                                                                                                       Sequence 67. Application US/07609716
Patent No. 5514501
GENERAL INFORMATION: Franco A.
APPLICANT: Ferrarl, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 551458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ROWLAND, BEFTLAM I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-7881-7989
TELEPHONE: 415-7388-73249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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APPLICATION NUMBER: US/07/609,716 FILING DATE: 06-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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4 GSFGGS 9
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                                                             COUNTRY:
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                                      ZIP: 94111
                                                                             San Francisco
CA
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  Floppy disk
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Pred. No.
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SEQUENCE CHARACTERISTICS:
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
                APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-0CT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
                                                                                                                                                                                                      APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John w
APPLICANT: Dorman, Mary A
TITILE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITILE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0:
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                   APPLICATION NUMBER: US 08/175,155 FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 83.3%;
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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REFERENCE/DOCKET NUMBER:
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amino acid
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04-NOV-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 CORPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES: PATENTION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                        APPLICATION NUMBER: US 01
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
                                                                                         APPLICATION NUMBER: US 01
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                           APPLICATION NUMBER: US 07/114,618 FILING DATE: 29-OCT-1987 PRIOR APPLICATION DATA:
                          ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                 APPLICATION NUMBER: FILING DATE: 29-DE
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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hes 5; Conserv
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Trecartin, Richard F
REGISTRATION NUMBER: 31,80
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Crissman, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Causey, Stuart
Pollock, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson, c....
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                                                                              US 08/175,155
                                                                                                                             US 08/053,049
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Pred. No.
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989

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US-08-475-411A-16
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Best Local :
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                                                                   TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM PC COMPALIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release $1.0, Version $1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,411A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F,
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-80V-1990
PRIOR APPLICATION DATA: US 07/269,429
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-00V-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Synthetic Protein Polymer
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
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TELEPHONE: 415.781-1989
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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Local Similarity 83.3%;
hes 5; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 06/927,258 FILING DATE: 04.NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Plehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                LENGTH: 15 amino acids TYPE: amino acid acid RANDEDNESS: single
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POPOLOGY:
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Pred. No.
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Query Match
Best Local Similarity
""+" 5; Conserve
                                                                                                     ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-475-411A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/08475411A Patent No. 6140072
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Best Local Similarity 83.3%;
Matches 5; Conservative
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APPLICATION NUMBER: US 07/269,429

FILING DATE: 09-MOV-1988

PRIOR APPLICATION NUMBER: US 07/114,618

APPLICATION NUMBER: US 07/114,618

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                             TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-180V-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 06/9
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Functional Recombinantly Prepared TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ferrari, Franco APPLICANT: Cappello, Joseph
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,801
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                                                                                                                                            linear
                                                                                                                      peptide
                                                                                                                                                           single
                                86.7%;
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              Score 26; DB 4;
Pred. No. 27;
0; Mismatches
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 Mismatches

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Pred. No. 27;
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1 GSLGGS 6

Conservative

Db 4 GSFGGS 9

Search completed: February 4, 2002, 08:01:38 Job time: 82 sec

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Title:
Perfect score:
Sequence:
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No.
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Maximum
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                                                  GENERAL INFORMATION:
APPLICANT: Scinneck, Jonathan
APPLICANT: O'Herrin, Sean
TITLE OF INVENTION: Molecular
TITLE OF INVENTION: Modify Im
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NAME: Kagan, Sarah A.
REGISTRATION UNDER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)508-9100
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HYPOTHETICAL: NO
FRAGMENT TYPE: diternal
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 1961 peptide linker
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MEDIUM TYRE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC POS/ANS-DOS
SOFTWARE: BALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RELIGIOATION DATA:
LING DATE: 28-MAR-1997
CLASSIFICATION: 314
CCLASSIFICATION: 314
CCLASSIFICATION: 314
CCLASSIFICATION: 314
                 CORRESPONDENCE ADDRESS:
                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Soluble Divalent and Multivalent TITLE OF INVENTION: Heterodimeric Analogs of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schneck, CAPPLICANT: O'Herrin,
                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1001 G 50
CITY: Washington
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                           1 GGGTSG 6
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                                                                                                                                                                                                                                                          GGGTSG
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Banner & Witcoff
                                                                                                                                                                                                                                                                                                                                                100.0%;
                                   Modify Immune Responses
20
                                                                    Molecular Complexes Which
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Pred. No. 1.6e+05;
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Best Local Similarity
6; Conserv
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US-09-063-276-10
                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08974546 Patent No. 5945287 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,712
EILING DATE: 28-MAR-1997
APPLICATION NUMBER: 60/014,367
EILING DATE: 28-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jes
APPLICANT: Lal, Preeti
APPLICANT: Corley, Nei
APPLICANT: Shah, Purvi
          APPLICATION NUMBER: US/08/974,546 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                          SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TELEPHONE: 202-508-9100
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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ZIP: 20001
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CITY: Washington
                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                      COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CO
OPERATING SYSTEM:
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APPLICATION NUMBER
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REGISTRATION NUMBER:
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Corley, Neil C.
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2071
TYPE: PRT
ORGANIUM: Ashbya gossypli
US-09-415-522-6
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US-08-461-990B-14
; Sequence 14, Application US/08461990B
: Patent No. 5851810
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Best Local Similarity
Thehes 6; Conserve
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APPLICANT: Gaffney, Thomas
APPLICANT: Hendland, Juergen
APPLICANT: Hillpsen, Peter
TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth
TITLE OF INVENTION: Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserva
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                                             GENERAL INFORMATION:
APPLICAMT: JOHN S. BLANCHARD
TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/415,522A
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 28
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENCTH: 348 amino acids
TYPE: amino acid
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LIBRARY: BRAITUT21
CLONE: 2525691
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TELEPHONE: 650-855-0555
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         199 GGGTSG 204
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TOPOLOGY: linear
                    STREET:
                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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  NEW YORK
                 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 33; DB 4; llarity 100.0%; Pred. No. 9.1e+02; Conservative 0; Mismatches 0;
                                     AMSTER, ROTHSTEIN & EBENSTEIN
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Pred. No. 1.9e+02
); Mismatches 0
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US-08-461-990B-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 26, Application US/08461990B
; Patent No. 5851810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local 9
          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461
FILING DATE: JUNE 5. 1995
ATTORNEY_AGRETY INFORMATION:
REGISTRATION NUMBER: 42.287
REFERENCE_POCKET NUMBER: 9670
TELEPHONE: (21.2) 697-595
TELEPHONE: (21.2) 697-595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII

                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:

DESCRIPTION: PROTEIN

HYDOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: B. STEAROTHERMOPHILUS
INDIVIDUAL ISOLATE: ALANINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/461,990B
FILING DATE: JUNE 5, 1995
ATFORNEY/ACENT INFORMATION:
NAME: CERAIG J. ARNOLD
REGISTRATION NUMBER: 34,287
REFERENCE/DOCKET NUMBER: 96700/370
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10016
                                                                                                                                                                                                                                                                                                       STREET: 90 PARI
CITY: NEW YORK
STATE: NEW YORK
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hes 5; Conserv
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(212) 286-0854 or 286-0082
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                                                    96700/370
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Pred. No.

    Mismatches

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Length 32; Indels

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Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09028934 Patent No. 6117670
                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 29:
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INFORMATION FOR SEQ ID NO: 26:
                                                                                                       NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS: LENGTH: 537 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                               APPLICATION NUMBER: US 08/258,261 FILING DATE: 08-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-007-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hammer, Philip E.
APPLICANT: Kirner, Sabine
APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: B. STEAROTHERMOPHILIS
INDIVIDUAL ISOLATE: ALANINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ligon, James M. APPLICANT: Hill, Dwight S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/028,934 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
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                                                                                                                                             CGC1506/CIP7
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Best Local S
Matches 5
          12 GGGTAG 17
                                               1 GGGTSG 6
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US-08-258-261B-2
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Best Local Similarity 83.3%;
                                                                                                                                                           TELEFAX: 919-541-8689
                                                                                                                                                                                                                        FILING DATE: 08-JUN-1944
CLASSIFICATION: 801
PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 08/457,205
ETLING DATE: 01-JUN-195
ATTORNEY, JGENT INFORMATION:
REGISTRATION NUMBER: 05-129
REGERENCY, DOCKET NUMBER: 061 1506/0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hammer, Phillip E
APPLICANT: Unces, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis
TITLE OF INVENTION: antiputhogenic substance
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/258,261B
                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                            TELEPHONE: 919-541-8614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 7 Skylin
                                                                                                TOPOLOGY:
                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10532
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                                                                                                             amino acid
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                                                                                                                          538 amino acids
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Beck, James Joseph
Hill, Dwight Steven
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  90.9%;
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Score 30; DB 1;
Pred. No. 7.9e+02;
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Pred. No. 7.9e+02;
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               Length 538;
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Conservative

Mismatches

Indels

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US-08-457-342-2
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                                                                                                 Sequence 2, Applic
Patent No. 5662898
                                                                                                                                                                                                                                                                                       Matches
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Patent No.
                                                                                  GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                              APPLICANT:
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release 1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-7UN-1995
CLASSIFTCATON: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Clba-Geigy Corporation
STREET: 7 Skyline Drive
            APPLICANT:
                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hammer, Phillip E.
APPLICANT: Unes. Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
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12 GGGTAG 17
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nes 5; Conservative
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FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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                                                                                                                     Application US/08457342
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       Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
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Ligon, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                    Score 30; DB 1;
Pred. No. 7.9e+0
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                    9e+02
                                                                                                                                                                                                                                                                                                                      Length 538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                             GENERAL
                                                                                                                           APPLICANT: Schupp, Thomas APPLICANT: Ligon, James M. APPLICANT: Ligon, James M. Steven APPLICANT: Hill, Dwight Steven APPLICANT: Ryals, John Andrew APPLICANT: Gaffney, Thomas Deane APPLICANT: Lam, Stephen Ting APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 919-541-86:
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                 APPLICANT: Lam, Stephen fing
APPLICANT: Hanmer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TVEE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease 1.0, Version $1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lam. Stephen Ting
APPLICANT: Hammer, Philip B.
APPLICANT: Utnes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/457,:

FILING DATE: 01-JUN-1995

APPLICATION NUMBER: 08/258,261
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CITY: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                           hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                         12 GGGTAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
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STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                           INFORMATION:
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    538 amino acids
amino acid

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                                                                                                                                             Gaffney, Thomas Deane
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Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip E.
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Ciba-Geigy Corporation
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    Mismatches

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Pred. No. 7
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7.9e+02;
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GENERAL INFORMATION:
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Matches 5; Conserv
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYA:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                        APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF IMVENTION: Genes for the synthesis of
TITLE OF IMVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GGGTAG 17
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                                                                                       ZIP: 10532
                                                                                                       COUNTRY:
                                                                                                                                         CITY: Hawthorne
                                                                                                                                                          ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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Gaffney, Thomas Deane
Lam, Stephen Ting
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Beck, James Joseph
Hill, Dwight Steven
                                                                                                          USA
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Pred. No. 7.9e+02;
1; Mismatches 0;
  Version #1.25
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FILING DATE: 01-JUN-1995

CLASSIPICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/457,205

APPLICATION NUMBER: US 08/25,261

FILING DATE: 08-JUN-1995

APPLICATION NUMBER: 08-JUN-1995

APPLICATION NUMBER: 08-JUN-1995

APPLICATION NUMBER: 08-JUN-1995

APPLICATION NUMBER: 08-JUN-1995

REPERBACK/DACKET NUMBER: 51.29

REPERBACK/DACKET NUMBER: 0CGC 1506/C1

TRELEPHONE: 919-541-8619

TRELEPHONE: 919-541-8619

TRELEPHONE: 919-541-8619

INFORMATION FOR SED JUNO: 2:
SEQUENCE CHARACTERISTICS: 108-JUN-1995

INFORMATION FOR SED JUNO: 2:
TRELEPHONE: 1988 animo senids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08457335A
Patent No. 5723759
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                                                                                                                                                                                                                ZIP: 10532

COMPUTER READABLE FORM.
MEDIUM TYPE: PIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SUSTEM: P-TOS/MS DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-7UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-7UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                FILING DATE: 01-JUN-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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Local Similarity 83.3%;
hes 5; Conservative
                                                                                                                                                              APPLICATION NUMBER: US/08/457,335A
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hawthorne
STATE: NY
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
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Beck, James Joseph
Hill, Dwight Steven
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01-JUN-1995
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Pred. No. 7.9e+02;
1; Mismatches 0;
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; MOLECULE TYPE: protein US-08-729-214-2
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                  Query Match 90.9%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local :
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                                                                                                                                                                                                                                                   TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
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PILING DATE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFIC
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MEDIUM TYPE: Ploppy disk
COMPUTER: HAM PLOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hammer, Phillip
APPLICANT: van Pee, Karl-E
APPLICANT: Kirner, Sabine
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APPLICANT:
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                                                                                                                                                                                                                   LENGTH: 538 amino acids
TYPE: amino acid
                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 520 Whit
CITY: Tarrytown
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nes 5; Conserv
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGTSG 6
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amino acid
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Hill, Dwight Steven
Hyals, John Andrew
Hammer, Phillip B.
Van Pee, Karl-Heinz
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              Score 30; DB 2; L, Pred. No. 7.9e+02; L; Mismatches 0;
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Pred. No. 7.9e+02;
                                                             Length 538;
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              Indels
          0,
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          Gaps
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          0;
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                                                                                                                                                                                                                                 RESULT 16
US-09-028-934-2
; Sequence 2, Ap
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US-08-729-214-24
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                                                                                                                                                                                                               Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 919-541-8587
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
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                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: MAGENT INFORMATION:
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELLECOMMINICATION INFORMATION:
TELLETIONE: 919-941-9597
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APPLICANT:
APPLICANT:
                         APPLICANT:
APPLICANT:
APPLICANT:
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TOPOLOGY: line-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: 371
MUBBER OF SEQUENCES: 27
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                    12 GGGTAG 17
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FILING DATE: TBA
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CITY: Tarrytown
STATE: NY
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6117670
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Hammer, Philip E.
van Pee, Karl-Heinz
Kirner, Sabine
Young, Thomas R.
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                                                                                                  Ligon, James M.
Hill, Dwight S.
Lam, Steven T.
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Pred. No. 7.9e+02;
1; Mismatches (
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US-09-028-934-24
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APPLICATION NUMBER: US 08/729, 214

PILIAG DATE: 09-0CT-1996

PRIOR APPLICATION NUMBER: US 08/258, 261

PILIAG DATE: 08-JUN-1994

ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIM TYPE: FLOPPY disk
COMPUTER: LIM PC COMPARATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIAN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                             NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670art1s Corporation
                                                                                                                                                                      TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes TITLE OF INVENTION: Thereof
                                                                                                                                                                                                           APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
                                                                                                                                                                                                                                                                 APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Philip
COMPUTER READABLE FORM:
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CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/028,934 FILING DATE: CLASSIFICATION:
                                STATE: I
                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 30,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                  27709
                                                                        Research Triangle Park
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                                                                                             3054 Cornwallis Road
                                     USA
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Pred. No. 7.9e+02;
1; Mismatches 0; Indels
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; ORGANISM: Fusarium
US-09-199-229-2
RESULT 19
US-09-443-087-2
; Sequence 2, Application US/09443087
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                                                                                                                                            Query Match
Best Local Similarity
"~+^hes 5; Conserve
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EILING DATE: 08-20N-1944
ATTORNEY/ACENT INFORMATION:
NAME: M-4015, J. TIMOCHY
REGISTRATION NUMBER: 38-241
REFERENCE/DOCKET NUMBER: 050
TELEPONNE: 19.9-541-6687
TELEPONNE: 19.9-541-6687
INFORMATION FOR SEQ DATE: 050
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yaver, Debble S.
APPLICANT: Rey, Michael W.
APPLICANT: Rey, Michael W.
TITLE OF INVENTION: Activity and Nucleic Acids Encoding Same
FILE BETERKENE: 5735.000-US
CURRENT APPLICATION NUMBER: US/09/199, 229
CURRENT PILLO BATE: 1998-11-24
UNBER OF SED, DO NOS: 2010-00-13 0
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COMPUTER: IBM PC compatible
OPERNTING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release 1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 538 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                                                        20 GGGTAG
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                                                                                                                                                              Conservative
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                                                                                                                                                                               90.9%;
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                                                                                                                                                                               Score 30; DB 3; Length 543; Pred. No. 8e+02;
                                                                                                                                                                   Mismatches
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US-08-955-848A-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVERTION: Polypeptides Having Choline Oxidase
TITLE OF INVERTION: Activity And Mucketo Acids Encoding
FILE REFERENCE: 5735.200-US
CURRENT APPLICATION NUMBER: 05/09/443,087
CURRENT FILING DATE: 1939-11-18
RAKLER FILING DATE: 1939-11-12
UNBERT OF IND 13 1939-11-24
UNBERT OF ED 11 NOS: 2
SOPTMARE: FEASTSEQ for Windows Version 3.0
SEQ ID NO 2
**ENORMER CALLS**
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Best Local :
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/029,16
FILING DATE: 25-CCT-1997
ATTORNET/AGENT INFORMATION:
NAME: Bennett, Dennis A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6146864
GENERAL INFORMATION:
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APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTMARE. FESTED FOR WINDOWS VERSION 2.0 CURRENT APPLICATION NATA: US/08/955,848A FILING BOTE: UZ-0CT-1997 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION: 55 CT-597 CLASSILICATION:
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PRIOR APPLICATION UNBER: 60/029,165
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APPLICANT: Feng, Yiqing
TITLE OF INVENTION: NO. 5969105
TITLE OF INVENTION: Agonists
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                                                                                                                                                                                                                             TELEFAX:
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COMPUTER: IF
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hes 5; Conserv
     STRANDEDNESS:
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5969105
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                                                                                                                                                                                                                             314-737-6972
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single
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83.3%;
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                                                                                                                                                45:
                                                                                                                                                                                                                                                                                                                               C-2992/1
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              Sequence 2, Application US/08256156A
Petent No. 5837021
GENERAL IMPORMATION:
APPLICAMIT; Nu. Anna M.
TITLE OF INVENTION: No. 5837821e
UNIMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                           US-08-256-156A-2
                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                            US-08-501-253A-9
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Best Local Similarity by...
""" tohes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION: 512-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARER PATENTION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Retileberger, Denise M.
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Uckun, Fatih
APPLICANT: Tumer, Niigun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAp and PAP Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/501,253A FILING DATE: 11-JUL-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Minneapolis
STATE: MM
                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                  1 GGGTSG 6
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                                                                                                                                                                                                                                                                                                                                                        linear
Rothwell, Figg, Ernst & Kurz, P.C
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                                                                                                                                                                                                                                                                                                                                       peptide
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83.3%;
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83.3%;
                                              5837821el Antibody Constructs
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47;
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US-08-377-687-39; Sequence 39; Application US/08377687
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APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CASSORN, RUPERT W.
APPLICANT: CSSORN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

APPLICATION WHENER: US/08/256,156A

FILING DATE: 24-JUN-1994
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
COMPUTER: ISM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
                                   CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 83.3%; hes 5; Conservation
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STRANDEDNESS
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                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                      CITY: WASHI
STATE: D.C.
                                                                                                                                                                                                                                                                                   STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                              FILING DATE:
                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN DARBY & CUSHMAN
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APPLICATION NUMBER: US 0 FILING DATE: 04-JAN-1993
                                                                                                                                                                                                                                   20005
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                  US 08/002,480
                                                                                                 US/08/377,687
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; MOLECULE TYPE:
US-08-777-192-39
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Best Local Similarity
Matches 5; Conserv
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TELEPAX: 202-822-9944
INFORMATION FOR SEQ. ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                       TELEPHONE: 202-861-30
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL N.
                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGEPT INFOWANTION:

NAME: KOKULIS PAUL N.

REDISTRATION NUMBER: 16.773

REDISTRATION NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC COMPATIBLE
COMPUTER: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHMAN
STREET: 1100 NEW )
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GGGSSG 29
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
                                     TOPOLOGY:
                                                 STRANDEDNESS
                                                                     TYPE: amino acid
                                                                                      LENGTH:
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                                                                                 42 amino acids
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OSBORN, RUPERT W.
REES, SARAH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                     linear
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                 peptide
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    Mismatches

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Pred. No. 1.2e+02;
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PCT-US96-01720-10 Sequence 10, Application PC/TUS9601720
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                                           RESULT 26
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                                                                                                                                                                                             Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08971982
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Best Local
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-661-3000
TELEFAX: 202-822-9944
INFORMATION OR SEO ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                           24 GGGSSG 29
                                                                                                                                                           Local Similarity
les 5; Conserv
                                                                                                              1 GGGTSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GGGSSG 29
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                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/002,480 FILING DATE: 04-JAN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BROEKAERT, WILLEM F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
5; Conserva
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
REES, SARAH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERRAS, FRANKY R.G
                                                                                                                                                                       87.9%;
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83.3%;
                                                                                                                                                                       Score 29; DB 4;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                         Mismatches
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                                                                                                                                                                                      Length 42;
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                                                                                                                                                       Indels
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                                                                                                                                                    0;
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CT-US96-01720-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MODITIFE OF INVENTION: MODITIFE OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                          REFERENCE/DOCKET NUMBER:
[NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION WIMBER: US 08/
APPLICATION WIMBER: US 08/
APPLICATION DATE: 09-PEB-1995
APPORNEY/AGENT INFORMATION:
NAME: PAIMBLES: SLEVEN M,
REGISTRATION NUMBER: 31,99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MODIFLE
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
LEDICH TYPE: Floppy disk
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan-
                                TOPOLOGY:
                                            STRANDEDNESS:
                                                                                                                                         NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
COMPUTER: II
                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GGGTGG 64
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                                                            amino acid
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amino acid
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                                linear
             protein
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83.3%;
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Pred. No. 1.9e+02;
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                                                                                 US-08-481-658B-50
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Best Local Similarity
Thehes 5; Conserv
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                                                                                                   RESULT 29
                                                                                                                                                                                                                                                                                                      US-08-325-253-10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION MUNEER: PCT/EP 93/00908
FILING DATE: 15-April-193
PRIOR APPLICATION MUNEER: England 9209032.3
FILING DATE: 25-April-1992
ATTORNEY/AGENT INFORMATION:
NAME: M. MULTRY CONT. 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.3%;
Matches 5; Conservative
                                                Sequence 50, Application US/08481658B Patent No. 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5686564
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10,
                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: W. MUITBY SPTUILL
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4.4
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Albert Schmitz
TITLE OF INVENTION: the Carboxy Terminal Sequence of Hirudin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Derek Edward BI
APPLICANT: Hans Rink
APPLICANT: Markus Gr(tter
APPLICANT: John Peter Prid
APPLICANT: Albert Schmitz
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CIBA-GEIGY Corporation
STREET: p.O. Box 12257
CITY: Research Triangle Park
STATE: No. 5686564th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GGGTGG 64
                                                                                                                                                    71 GGGTKG 76
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/325,253
FILING DATE: 20-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                       91 amino acids
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Zavada, Jan
Pastorekova, Silvia
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   87.9%;
83.3%;
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0; Mismatches 1;
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                                                                                                                                                                                                                                   Score 29; DB 1;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                   Length 91;
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US-08-477-504A-50
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    Sequence 50, Application US/08477504A Patent No. 5972353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-435-203
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lin
MOLECULE TYPE:
DESCRIPTION:
DESCRIPTION:
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STREET: v ...
CITY: Tiburon
California
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: US/08/477,504A
                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lauder, Leona L. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                      ADDRESSEE: Leona L.
emmret: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GGGSSG 18
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                                                                                                                       ZIP: 94920
                                                                                                                                   COUNTRY:
                                                                                                                                                     STATE:
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                                                                                                                                                     California
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                                                                                                                                     USA
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                                                                                                                                                                                                                                                      K, Jaromir
MN Gene and Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.98;
83.38;
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    Mismatches

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Pred. No. 2.5e+02;
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US-08-486-756A-50
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                                                                                                                                                                 COMPUTER NEADMBLE FORM:
MEDIUM TIPE: PLOPBY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCITMARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNDERS: U5/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION HUMBER: U5/08/260,190
FILING DATE: 15-JUN-194
APTIONENCYGETT INFORMATION:
REVIEW LAUGHT, LEGNA L.
REVIEW LAUGHT, LEGNA L.
REVIEW LAUGHT, LEGNA L.
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Best Local :
                                         TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFERAX: 415-435-0727
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                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MN Gene and Protein
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Local Similarity B3.3%;
Res 5; Conservati
TOPOLOGY:
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                               ENGTH:
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Pred. No. 2.5e+02;
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; MOLECULE TYPE:
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; DESCRIPTION:
US-08-486-756A-50
Query Match
Best Local Similarity
Thehes 5; Conserv
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Best Local Similarity
Matches 5; Conserve
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TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                       TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvi
APPLICANT: Pastorek, Jaromir
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CITY: Tiburon
STATE: Califor
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                                                                                                      DESCRIPTION:
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
                                                                                                                                                                                                                                                                                           NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
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07-JUN-1995
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83.3%;
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                            Score 29;
Pred. No.
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Pred. No. 2
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                            DB 2;
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                                       Length 98;
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US-08-485-863A-50
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 15-JUN-1994
ATTORNEY/AGENT IMPORATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/TOKYET NUMBER: 30,863
                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                 APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOFFMANDER DESCRIPTION PC-DOS/MS-DOS
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APPLICANT: PASTOTEKOVA, SI1via
APPLICANT: PASTOTEK, Jaromir
TITLE OF INVENTION: MN Gene and Protein
                                                                                                                        NUMBER OF SEQUENCES:
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6 Mariposa Court
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6 Mariposa Court
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83.3%;
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    Mismatches

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Pred. No. 2.5e+02;
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                                             FILING DATE: 07-JUN-1995
CLASSFEICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-194
ATTORNEY-MCSHM TINDORMATION:
NAME: LBUGET, LEGNE L.
                                                                                                                                                                 SOFTWARE: Patentin Relacement APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
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APPLICANT: Pastorekova, Silvia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: D-
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GGGSSG 18
                               REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                              ZIP: 94104
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07-JUN-1995
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30,863

D-0021.3E

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Query Match 87.9%;
Best Local Similarity 83.3%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       DESCRIPTION: 1 chain
                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                           amino acid
                                                                                                                                                                                              98 amino acids
                                                                                                                                                                                                                                                 415-435-07
    Conservative
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                                                                                                                                                          linear
                                                                                                                 protein Region of homology to collagen alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/485,863A
                                                                                                                                                                                                                                                                                                                   30,863
                   Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                    D-0021.3G
    Mismatches
                     5e+02
                                 Length 98;
    Indels
    0
Gaps
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US-08-905-223-319
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: SUL STREET: SAN DIEGO CITY: SAN DIEGO CTATE: California
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPEAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92101-3505
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edwards, Jean-Baj
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
DESCRIPTION: Region of homology to collagen alpha
DESCRIPTION: 1 chain
                                                                                              FEATURE:
                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICAMP: LACTOIX, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                               TYPE: AMI
TOPOLOGY:
      NAME/KEY: sig_peptide
LOCATION: -39.-1
IDENTIFICATION HEHIOD: Von Heijne matrix
OTHER INFORMATION: socre 5,7
OTHER INFORMATION: seq SPAFILVAGPGWA/RP
                                                                                                                                                                                                                                                                                                                         NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 5; Conserv
                                                                                                              TISSUE TYPE:
                                                                                                                                 ORGANISM:
                                                                                                                                                                                          TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GGGSSG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCGTSG 6
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OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08905223
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                                                                                                                            Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415-981-2034
                                                                                                                                                            PROTEIN
                                                                                                              Brain
                                                                                                                                                                                                                                                                                                                                                                                 536
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83.3%;
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Pred. No. 2.5e+02;
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Query Match
Best Local Similarity
Thes 5; Conserve
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5252466-6
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; APPLICANT: CROWN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; YIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; FURIFYING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107, Application US/07956700B Patent No. 5539092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83...
""Frhes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PARENI ... CONTRACTION:
GENERAL INVENTION:
APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TTTLE OF INVENTION: Carboxylase
                                           TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA,
APPLICATION NUMBER: US/O7
FILING DATE: 18 MAY 1990
PRIOR APPLICATION NUMBER: 354,26
APPLICATION NUMBER: 354,26
APPLICATION NUMBER: 39407
                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19921002
                                                                                                                      CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5559092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                            SEQUENCE CHARACTERISTICS:
                                                                                       REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII-DOS
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                                                                        TELEPHONE:
               LENGTH:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                 60610
Amino acid
                                                                                                                                                                                                                                                                                                                                             Illinois
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321 No. 5539092th Clark Street
             123 amino acids
                                                                                                                                                                                                                                                                                                                                USA
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                                                                          1-312-744-0090
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                                                                                                                    33,268
                                                                                                         ARCD:058
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Pred. No. 2.7e+02;
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Pred. No. 2.6e+02;
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US-08-485-607-107

; Sequence 107, Application US/08485607

; Patent No. 5792627
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; MOLECULE TYPE: Peptide
US-07-956-700B-107
                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: Peptide US-08-476-537-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-476-537-107
                                                          RESULT 40
                                                                                                                                                                                            Query Match 87.9%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87,9%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PACENT NO. JULIANATION:
REPRIZION REPRIZION APPLIZIONNE ROBERT HASELKORN AND PLOT GOTNICK!
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
TITLE OF INVENTION: Carboxylase
"""" OF SEQUENCES: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27F: 66610

COMPUTER READABLE FORM:
MEDIUM TYPE: THE COMPUTER: LEM PC Compatible
OPERNTING SISTEM: PC-DOS/MS-DOS
SOFTMARE: ASCII-DOS
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APELICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. NO. 575629Chrup
REGISTRATION NUMBER: 33.268
REFERENCE/DOCKET NUMBER: ARCD:058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/476,537 FILING DATE:
                                                                                                                  1111 |
32 GGGTGG 37
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, White & Durkee STREET: 321 No. 5756290th Clark Street
                                                                                                                                                       1 GGGTSG 6
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                                                                                                                                                                                            Score 29; DB 1; Length 123; Pred. No. 3e+02; 0; Mismatches 1; Indels
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Pred. No. 3e+02;
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Search completed: February 4,
Job time: 80 sec
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Best Local Similarity
Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Standard Stand
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APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TITLE OF INVENTION: Carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET:
Chicago
CITY: Chicago
Illinois
TATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      32 GGGTGG 37
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A:Reference number: Z20231
A:Accession: T26555
A:Status:
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T26555
                                                                                                                                                                                                                  h/pothetical protein Y22F5A.5 - Caenorhabditis elegans C:Specias: Caenorhabditis elegans C:Date: 15-oct-1999 *sequence_revision 15-oct-1999 *te C:Accession: 726555
                                                                                                                                                                         R:Gardner, A.
submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upstroem stimulatory factor - human (fragment)
c;Species: Homo sapiens (man)
c;Date: 02-Jul-1996 #Sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
c;Accession: I54074
R.Sirito, M., Walker, S., Lin, Q.; Kozlowski, M.T.; Klein, W.H.; Sawadogo, I
Gene Expr. 2, 231-240, 1992
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A:Accession: I54074
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A; Residues: 1-234 < RES>
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A; Molecule type: DNA
A; Residues: 1-102 <SOU>
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R:Soulllard, N.; Magot, M.; Possot, O.; Sibold, C. Mol. Evol. 27, 65-76, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross*references: EMBL:X07500; NID:g44619; A;Note: the authors translated the codon CAG
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                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-279 <WIL>
                                   Experimental source: clone Y22F5A
                                                         Cross-references: EMBL:AL021479;
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Local Similarity 100.0%;
les 6; Conservative
CESP: Y22F5A.5
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C;Accession: T48493
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, i
                                                                                                                                                                                                                                         hypothetical protein T88J4.160 - Arabidopsis thaliana Cipecies: Arabidopsis thaliana (mouse-ear cress) Cipecies: Arabidopsis thaliana (mouse-ear cress) Cipecies: Arabidopsis thaliana (mouse-ear cress) Cipecies: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
A; Experimental source: C; Genetics:
                                            A; Cross-references:
                                                               A; Residues: 1-303 <BEV>
                                                                                      A; Molecule type: DNA
                                                                                                               A; Status: preliminary
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                                                                                                                                      A; Accession: T48493
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A; Residues: 1-289 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: DMBL.AC003028; NID:g3335356; PID:g3335373
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Woffet, K.S.; Cronin, L.A.; Shea, M.; Venkken, S.E.; Umayem, L.; Tallon,
euss, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Mature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-289 <ROU>
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A; Accession: T01257
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A;Introns: 1427
A;Introns: 1427
C;Superfamily: Caenorhabditis elegans hypothetical protein C02A12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: F16M14.18; At2g38250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g3335373; PIDN:AAC27174.1; GSPDB:GN00139
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                                         EMBL: AL163652
                   cultivar Columbia;
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Pred. No.
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                                                                                                                                                                                   S.; Bancroft,
April 2000
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                   clone T28J14
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A; Reference number: $3215
A; Accession: $32156
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-563 <CHE>
                              A;Cross-references: EMBL:X72617; NID:g288115; PC:Superfamily: alcohol oxidase
C;Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                 mandelonitrile lyase (EC 4.1.2.10) - black cherry C:Species: Prunus serotina (black cherry) C:Date: 22-Nov-1993 #sequence_revision 13-Mar-1997
                                                                                                                                                                                         A; Description: Nucleotide sequence
                                                                                                                                                                                                             submitted to the EMBL Data Library,
                                                                                                                                                                                                                                   C;Accession: S32156
R;Cheng, I.P.; Poulton,
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A: Residues: 1-504 - 4805-
A: Cross-references: GB:D64040; NID:g1020400; PID:d1011557; PID:g1020401
R:Jones, B.M.; Fetter, R.D.; Tear, G.; Goodman, C.S.
Cell 82, 1013-1023, 1995
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A57215
Splal coalls missing (gcm) protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10 Nov-1995 sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57215; A57216
R:Hosoya, T. Takizawa, K.; Nitta, K.; Hotta, Y.
Cell 82, 1025-1036, 1995
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C;Keywords: nucleus
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A;Molecule type: mRNA
A;Residues: 1-504 <JON>
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A.Introns: 67/1; 152/3; 201/3
A.Mote: T28J14.160
C;Superfamily: Arabidopsis thaliana hypothetical protein pt09039.6
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93;
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R;Breidt Jr., F.; Hengstenberg, W.; Finkeldei, U.; Stewart, J. Biol. Chem. 262, 16444-16449, 1987
                                    phosphorransferrase system enzyme II (EC 2.7.1.69), lactose-specific, factor C:Species: Staphylococcus aureus C:Date: 20-Jun-1989 #text_change 15-Oct-1999 C:Accession: BE8474
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X68497
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-569 <DET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Detheux, M.; Vandekerckhove, J.; van Schaftingen, FEBS Lett. 321, 111-115, 1993
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B23696
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Length 569;

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the regulatory protein

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for

the

lactose-specific components of the phosp

11

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glucokinase regulator - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Dec:1994 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                              A:MOLECULE type: DNA
A:Residues: 1-58 <DEV)
A:Cross-references: GB:M60447; GB:J05748; NID:g149404; PIDN:AAA25182.1; PID:g149411
C:Reywords: phosphotransferase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                   R;de Vos, W.M.; Boerrigter, I.; van Rooyen, R.J.;
J. Biol. Chem. 265, 22554-22560, 1990
A;Title: Characterization of the lactose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphotransferase system enzyme II (EC 2.7.1.69) - Lactococcus C;Species: Lettococcus lactis C:Bate: 04-Oct.1991 #sequence_revision 04-Oct.1991 #text_change
                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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A; Accession: B23696
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C. Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #. C. Accession: T50766 R. HH, 7.; Poulton, J.E. subnitted to the EMBL Data Library, January 1998 A. Reference number: 725225 A. Accession: T50766 A. Status: preliminary; translated from GB/EMBL/DDBJ.
                                                                                                                                                                                                                                                                                                     phosphotransferase system enzyme II (EC 2.7.1.69) - Lactobacillus casel C.Species: Lactobacillus casel C.Date: 04 -Oct-1991 *text_change 15-Oct-1995 C.Date: 04 -Oct-1991 *text_change 15-Oct-1999 C.Accession: B2369 R.Alpert, C.A.; Chassy, B.M. J. C.Accession: B2369 R.Alpert, C.A.; Chassy, B.M. J. Biol. Chem. 265, 22501-2256, 1990 A.7itle: Whocular cloning and DNA sequence of lacE, the gene encoding the lactic charge of the phosphorylation.
A.Reference number: A23697; NUID:91093108
A.Accession: B23697
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A. Arcession: B28474
A. Molecule type: DNA
A. Residues: 1-572 CBRED
A. Cross-references: GB:J03479; NID:g153031
C. Keywords: phosphotransferase
  RUSULT
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A Residues: 1-574 <HUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mundelonitrile lyase (BC 4.1.2.10) isoform MDL4 precursor [imported] - black cherry
C.Species: Prunus serotina (black cherry)
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Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
Accession: T50766
                                                                                                                                                                                                                    .Cross-references: GB:M60851; NID:g149561; PIDN:AAA72984.1; PID:g149563
.Keywords: phosphotransferase; transmembrane protein
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Best Local
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6; Conserv
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Pred. No. 1.7e+02;
Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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3. 1.7e+02;
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                                   A;Description: Human glucokinase
A;Reference number: S52485
A;Accession: S52485
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A;Map position: 2
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A; Reference number: Z24541
A; Accession: T48795
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R; Schulte, U.; Aign, V.; Hoheisel,
A; Molecule type: mRNA
                 A;Status: preliminary
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A:Gene: At2g42580
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A; Residues: 1-618 <STO>
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hypothetical protein At2942580 [imported] - Arabidopsis thaliana (souse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change C:Accession: F84855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: DNA
A:Rosidues: 1-578 <SCH>
A:Cross-references: EMBL:AL353822; GSPDB:GN00112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       origin recognition complex subunit 2 related protein (imported) - Neurospora crassa N;Alternate names: protein 1556.30 C:Species: Neurospora crassa C:Spate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Sequence Database, April 2000
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Pred. No.
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1.7e+02;
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                         #text_change 02-Feb-2001
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nterman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Rature 402, 761-768, 1999

A;Cross-references: GB:AE002093; NID:g4559333; PIDN:AAD22995.1; GSPDB:GN00139 A; Title: Sequence and analysis of chromosome 2 A; Reference number: A84420; MUID: 20083487 A; Accession: F84855 of the plant Arabidopsis thaliana

Score 33; DB 2; Le Pred. No. 1.8e+02; Indels 0 0

Length 618

glucokinase regulator - human G:Species: Homo saplens (man) C;Datus: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999 C:Accession: S52485 C:Accession: S52485 R:Bonthrow, D.T.; Intody, S.; Warner, J.P. R:Bonthrow, D.T.; Intody, S.; Warner, J.P.

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A: Residues: 1-62 < KLI>
A: Cross-references: GB: X05418; NID: g34040; PIDN: CAAZ8991.1; PID: g34041; GB: X05419; NID: g42040; A: Cross-references: GB: X05418; NID: g34042; PIDN: CAAZ8995.1; PID: g1335194; GB: X05421; NID: g3404
A: Mote: the unbors translated the codon Acc for residue g3 as Asp and ACA for residue g4. Note: the unbors translated in sort annotated in GenBank entries HSKER65A, HSKER65A; S mistranslated as A Met Initiator codon
C: Genetics: The complete translation is not annotated in GenBank entries HSKER65A, HSKER65A; Cenetics: The complete translation is not annotated in GenBank entries HSKER65A; HSKER65A; MSKER65A; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER6SB; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSKER65B; MSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  keratin, 65K type II cytoskeletal - human C:Specias: impo sapiens (man) C:Specias: long sapiens (man) C:Date: 31-Dec:1986 Sequence_revision 30-Sep-1991 #text_change 20-Jun-2000 C:Accession: A:29668 Sequence_revision 30-Sep-1991 #text_change 20-Jun-2000 R:Kilinge b.H.; Sylvestre, Y.R.; Froedberg, I.M.; Blumenberg, M. J. Holis Boll. 24, 313-329, 1987
A:Filte: Broultdon of Keratin genes: different protein domains evolve by difference number: A29666; MUID:87254239
                                                                                                                                                                                                      A:Introns: 215/3; 289/2; 309/3; 341/3; C:Superfamily: cytoskeletal keratin C:Keywords: coiled coil
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C:species: Rattus morregicus (Norway rat)
C:Date: 10-Sep-1999 sequence_revision 10-Sep-1999 stext_change
C:Accession: S41745
E:Detheux, M. Vandekerckhove, J.: van Schaftingen, E.
FEBS Lett. 339, 312-315, 1994
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A:Residues: 1-627 <DET>
C:Superfamily: glucokinase regulator
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A.Accession: $41745
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C;Superfamily: glucokinase regulator
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A;Residues: 1-625 <BNBL:248475; NID:9683571; PIDN:CAA88367.1; PID:9683572 C;Genetics:
                                                    Query Match
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Pred. No. 1.9
0; Mismatches
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Pred. No. 1.9
); Mismatches
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                                        DB 2;
1.9e+02;
0;
                                                                                                                                                                                                                                                   438/3; 512/2; 525/1
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A; Introns: 30/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
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Best Local
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                                                                                                                                                                                                                                           64 GGGTSG
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A;Cross-references: EMBL;X11403; NID:459591; FIDN:CAA35411.1; PID:91780830
A;Mote: possible protein-cooling frames are given
A;Note: Libe DNA sequence was submitted to EMBL, December 1989, In computer
                                                                                                                                                                                                                                                                                                                                A;Title: Analysis of the protein-coding content of the sequence of A;Reference number: 809749; MUID:90269039
A;Accession: 809815
                                                                                                                                                                                                                                                                                                                                                                                                                          A.Note: host Homo Sapiens (man)
C:Date: 31-Dec-1900 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: S09815
R:Chee, M.S.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; H
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-668 < CHE>
                                                                                                                                                                                                                                                                                                                                                                                               M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169,
                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: human cytomegalovirus, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: HFRF1 protein
422 GGGTSG
                                                                             Local Similarity
hes 6; Conserv
                                   1 GGGTSG 6
                                                                                                                                                                                varicella-zoster virus gene 26 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human cytomegalovirus (strain AD169)
                                                                                Conservative
                                                                                               100.0%;
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Pred. No.
                                                                             Mismatches
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                                                                                               2e+02;
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                                                                       Gaps
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submitted to the EMBL Data A:Reference number: Z20444 hypothetical protein 2K662.3 - Caenorhabditis elegans C:Species: Coenorhabditis elegans C:Date: 15-Oct\_1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000 A; Residues: 1-780 <WIL> A:Status: preliminary; translated from GB/EMBL/DDBJ EMBL: Z79604; PIDN: CAB01900.1; GSPDB: GN00028; clone 2K662 Library, August

Similarity 6 Conservative 56/1; 98/3; 176/3; 100.0%; 0, Score 33; DB 2; Pred. No. 2.3e+02; Mismatches 0; 206/3; 289/2; 311/1; 341/3; 444/3; Length 780 0, Gaps 507/3; 655/1; 0

69

endopeptidase Clp (EC 3.4.21.-) ATP-binding chain cd4B, chloroplast N;Alternate names: ATP-dependent Clp proteinase regulatory chain B; N;Contains: adenosinetriphosphatase (EC 3.6.1.3) C;Species: Lycoperation esculentum (tomato) (C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 19-3 C;Accession: B35905 [similarity]
CD4B protein ö

#text\_change 19-Jan-2001

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A:Gene: cd4b
A:Map position: 12
C:Function:
A:Description: allows clpP to hydrolyze polypeptides and proteins
e activity; AFP hydrolysis is required for clp hydrolysis of prot
C:Maperially: endopeptides c.p AFP-binding chain
C:Mayords: AFP; chloroplast: hydrolase; molecular chaperone; nuc
E:300-307/Region: nucleotide-binding motif B (P-loop)
F:31-737/Region: nucleotide-binding motif B (P-loop)
F:711-715/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
A; Gene: cd4A
A; Map position: 3
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Description: allows clpt to hydrolyze polypeptides and proteins, probably a activity. ATP hydrolysis is required for C.Lp hydrolysis of proteins but no C; superfamily: endospetidase CLp ATP-binding chain chaptering to the C. Reywords: ATP; chloroplast; hydrolase; molecular chaperone; nucleotide bin F, 302-309/Region: nucleotide-binding motif 8 (P-loop) F, 367-371/Region: nucleotide-binding motif 8 (P-loop) F; 107-717/Region: nucleotide-binding motif 8 (P-loop) F; 711-715/Region: nucleotide-binding motif 8 (P-loop) F; 711-715/Region: nucleotide-binding motif 8 (P-loop) Rightinding site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding Site: ATP (Lys) **status** predicted P: 308-711 ATP (Righting Motif B) Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding Rightinding
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Proc. Natl. Acad. Sci. U.S.A. 87, 3513-3517, 1990 
A:Title: Conservation of the regulatory subunit for the Clp A 
A:Reference number: A35905; MUID:90239044 
A:Accession: B35905
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A; Residues: 1-926 <GOT>
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Proc. Nbtl. Acad. Sci. U.S.A. 87, 3513-3517, 1990
A;Title: Conservation of the regulatory subunit for the Clp ATP-dependent protea A;Reference number: A35905; MUJD:90239044
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C;Genetics:
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A; Residues: 1-923 <GOT>
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                                                  246 GGGTSG 251
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ilarity 100.0%;
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Pred. No.
                                                                                                                                                                                                                                                     Score 33; DB 1;
Pred. No. 2.7e+02;
; Mismatches 0;
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A; Residues: 1-487,536-1192 <WIL4>
A; Cross-references: EMBL:296102; PIDN:CAB54262.1;
                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella A;Reterence number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number a;Accession: E82669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30s ribosomal protein 59 xr1536 [imported] - Xylella fastidiosa (strain 9a5
C:Specias: Xylella fastidiosa
C:Date: 18 Aug-2000 | sequence_revision 20-Aug-2000 | text_change 02-Sep-2000
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A; Cross-references: GB: AE003983; A; Experimental source: strain 9a
                                                                                             A; Molecule type: DNA
A; Residues: 1-130 <SIM>
                                                                                                                                                                                                  A; Status: preliminary
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Nature 406, 151-157, 2000
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clone H39E23

GSPDB:GN00023; CESP:H39E23.1b

23

E82669

Consortium of the Organization for

Nucleotide

reference number

A59328 below

B3; GB:AE003849; NID:g9106567; PIDN:AAF84345.1; GSPDB:GN 9a5c

1 GGGTSG

106 6 100. nilarity 100. Conservative

0.0%;

0 Score 33; Pred. No.

3.4e+02; hes 0; DB 2;

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0,

Length 1192;

kinase, short sp long splice form

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C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C:Accession: T18611; T18610; T23144; T23143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues; 1-1192 <WILL>
A;Cross:references: EMBL;281027; PIDN:CAB54179.1;
                                                                              A; Molecule type: DNA
A; Residues: 1-1192 <WIL3>
A; Cross-references: EMBL: 296102; PIDN: CAB54263.1;
A; Cross-references: EMBL: 296102; PIDN: CAB54263.1;
                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                              R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-487,536-1192 <WIL2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: Z18997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; McMurray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable serine/threonine-specific protein kinase (EC 2.7.1.-),
N;Contains: probable serine/threonine kinase, short splice form
A;Status: translated from GB/EMBL/DDBJ
                    A; Accession: T23143
                                                 A; Experimental source: clone H39E23
                                                                                                                                                                     A:Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                       A; Accession: T23144
                                                                                                                                                                                                                               A; Reference number: 219696
                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone AH10
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$70890
hypothetical protein b2674 - Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Date: 10 Sep-1999 #sequence_revision 10-Sep-1999 #to
C.Accession: $70890; C65047
R.JOrdan, A.; Aragall, E.; Gibert, I.; Barbe, J.
Wol. Microbiol. 19, 777-790, 1996
A.Title: Promoter identification and expression analys
A.Reference number: $70890; MUID:96417857
A.Accession: $70890
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Frana, J.S.; Franca, S.C.; Franco, M.C.; Brohn
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig;
chado, M.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, F.
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracoa, E.C.; Myaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.
Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.Y.; Savasa,
M.; Miracoa, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almcida, S.; Vettore, A.L.; Z
A; Reference number, A59328
A; Concents: annotation
Coenetiss.
     hypothetical protein nrdI [imported] - Escherichia C.Species: Bacherichia coli C;Date: 16:Feb-2001 #sequence_revision 16:Feb-2001 C;Accession: D#5515 Fundent III, G.; Burland, V.; Mau, R;Ferra, N.T.; Plunkett III, G.; Burland, V.; Mau,
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A;Accession: C65047
A;Status: preliminary; nucleic acid seque
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A;Mclecule type; DNA
A;Residues: 1.136 <JOR>
A;Residues: 1.136 <JOR>
A;Cross: references: EMBL:X79787; NID:g1050468; PIDN:CAA56185.1; PID:g1050471
R;Blatther, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
A; Rose, D.J.; Mau, B.; Shao, Y.
Sclence 277, 1453-1463, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
BRIONES, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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A; Residues: 1-136 <BLAT>
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1; Mismatches
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                                                                             #text_change 31-Mar-200:
           B.; Glasner,
                                                                                                                                                                     coli (strain 0157:H7)
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           J.D.; Rose,
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           D.J.;
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F84182
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A;Note: T2J13.80
C;Superfamily: Escherichia coli ribosomal
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N.Alternate names: protein 72/13.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
A. Fah-2000 stext_change 18-Feb-2000
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85915
A;Title: Genome sequence of Halobacterium species NRC-1.
A;RetErence number: A84160; MUID:20504483
A;Reteasion: FB41B2
A;Actatus: preliminary
A;Molecule type: DNA
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C;Superfamily: Bacillus subtilis conserved hypothetical protein
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-136 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Date: 02-Feb-2001 #sequence_revision
C:Accession: F84182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Vng0219h [imported] - Halobacterium sp. C; Species: Halobacterium sp. NRC-1
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A; Residues: 1-143 < RIE>
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A;Accession: T46122
A;Status: preliminary
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5; Conser
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Pred. No.
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Pred. No. 1.4e+02;
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R:Goddemcier, M.L.; Wulff, D.; Peix, G.
Plant Mol. Biol. 36, 795-802, 1998
A:Title: Root-specific expression of a Zea mays gene encoding a
A:Reference number: Z14904; MUID:98187261
A:Accession: 703371
                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine-rich protein grp3 - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein YILO55w - yeast (Saccharomyces cerevisiae)
NALtorante names: hypothetical protein J1148
C:Species: Saccharomyces cerevisiae
C:Date: 08-JUL 1995 #sequence_revision 08-Sep-1995 #text_change 08-Oct-19
C:Accession: $56827
  RESULT
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A:Experimental source: strain DK105; root
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C: Superfamily: yeas
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A; Residues; 1-245 <TOV>
A; Cross-references: EMBL: Z49330; NID:g1008194;
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submitted to the Protein Sequence Database,
A:Reference number: S56793
A:Accession: S56827
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C;Genetics:
A;Gene: VNG0219H
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A:Residues: 1-256 <GOD>
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Matches 5
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Best Local
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Best Local
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5; Conser
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                                                        97
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:AE004437; NID:g10579866; PIDN:AAG18826.1; GSPDB:GN00138
                                                                                                                                           90.9%;
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                                                                                                                       Score 30; DB
Pred. No. 2.6e
1; Mismatches
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Pred. No. 1.9e
1; Mismatches
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Pred. No.
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2.5e+02;
0;
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1.9e+02;
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                                                                                                                                                            DB 2;
                                                                                                                                           .6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein entJ [imported] - Escherichia coli (strain 0157:H7)
C.Spacelas: Escherichia coli
C.Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C.Accession: 685887
R.Petrab, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
              A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12
A:Reference number: A64720; MUID:97426617
                                                                                C; Accession: E65020
R; Blattner, F.R.; Plunkett III,
                                                                                                                  C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
                                                                                                                                                       ethanolamine utilization protein EutJ -
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A; Residues: 1-278 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A85480; A; Accession: G85887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta
Nature 409, 529-533, 2001
A. Title: Genome sequence of enterohemorrhagic Escherichia
A.; Reference number: A85480; MUID:21074935; PMID:11206551
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A;Gene: DR2232
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A; Residues: 1-276 <WHI>
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A;Accession: F75300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: F75300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - Deinococcus radiodurans (strain Rl)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
A:Accession: E65020
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Best Local
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6, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                    Similarity
5; Conser
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                     90.9%;
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                                                                                                                                                                                                                                                                                                                                     Score 30;
Pred. No.
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Pred. No.
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                                                                                   C.A.;
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2.8e+02;
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T.; Zalewski,
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                                                                                   Riley,
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, K.; Apoda
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Apoda

not shown

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                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1997
A:Reference number: Z19327
A:Accession: T20807
A:Status: preliminary, translated from GB/EMBL/DDBJ
A:Molecule type: DMA
A:Residues: 1-340 <WILD
                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F1347.1 - Caenorhabditis elegans C:Species: Cenorhabditis elegans C:Species: 15-Oct_1999 #sequence_revision 15-Oct_1999 #text_change 15-Oct_1999
                                                                                                                                                A;Gene: CESP:F13A7.1
A;Map position: 5
A;Introns: 6/2; 44/2;
                                                                                                                                                                                                                   A;Cross-references: EMBL:Z93377; PIDN:CAB07573.1; GSPDB:GN00023; CESP:F13A7.1
                                                                                                                                                                                                                                                                                                                                  R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                C; Accession: T20807
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A:Residues: 1-310 GND/
A;Cross-references: GB:AF002241; NID:92196706; PIDN:AAC38059.1;
C;Reywords: carbon-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Bruehlmann, F.; Keen, N.T.
Gene 202, 45-51, 1997
A;Title: Cloning, sequence and expression of the
A;Reference number: JC6502; MUID:98087416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pectate lyase (BC 4.2.2.2) - Amycolata sp.
C:Species: Amycolata sp.
C:Date: 16-ull-1999 #sequence_revision 16-Uul-1999 #text_change 21-Uul-2000
C:Accession: JC6502
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A; Status: preliminary
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                                              1 GGGTSG 6
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Pred. No. 3.4e+02;
l; Mismatches 0;
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ndent dehydrogenases.
A;Reference number: A34261; MUID:90254112
A;Accession: B34261
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Rickuroda, S.; Tanizawa, K.; Sakamoto, Y.; Tanaka, H.; Soda, K.
Biotemistry 9, 1009-1015, 1990
A;Title: Alanine dehydrogenases from two Bacillus species with distinct thermostabili
                                                                                  alanine dehydrogenase (EC 1.4.1.1) - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 11-Jun-1999
C;Accession: B34261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: maf transforming protein; maf homology F;259-348/Domain: maf homology <MAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S74567; NID:g807054; PIDN:AAB32820.1; PID:g807055 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c: Maf protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: 157555
R:Kurschner, C: Morgan, J.1
Mol. Cell #Biol. 15 246-254, 1999
A:Telte: The mmfer 157555; MUID: 55097997
A:Recession: 157555; MUID: 55097997
A:Recession: 157555; MUID: 55097997
A:Recession: 157555
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G:Species: Streptomyces coelicolor
G:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: 734954
R:Saunders, D.C: Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: murG; SCOEDB:SC4A10.17c
C;Superfamily: murG protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
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Pred. No. 3.7e
l; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAB51993.1; GSPDB:GN00070; SCOEDB:SC4A10.17c
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                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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3.7e+02;
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C; Genetics:
A; Gene: Lmx-1
A; Gene: Lmx-1
C; Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat hor; Superfamily: transcription regulation; zinc; Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc; F; 35-85, Donatin: LIM metal-binding repeat homology <LIMI>F; 94-147/Domain: LIM metal-binding repeat homology <LIM2>F; 94-147/Donain: homeobox homology <HOX>
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A:Molecule type: DNA
A:Residues: 1-372 <KURD
A:Cross-references: GB:M33299; NID:g142454; PIDN:AAA22211.1; PID:g142455
C;Superfamily: alanine dehydrogenase; alanine dehydrogenase homology
C;Reywords: NAD; oxidoreductuse
F:1-277/Domain: alanine dehydrogenase homology <ALAD
F:170-198/Region: beta-alpha-beta NAD nucleotide-binding fold
                                                                                                                                                                                                                hypothetical protein #16M2.50 - Arabidopsis thaliana G:Species: Arabidopsis thaliana G:Species: Arabidopsis thaliana (mouse-ear cress) G:patc: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 R;Accession: T46109 R;Accession: Meller-Auer. S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000 A:Reference number: Z24459 A;Accession: T48109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription factor inx.1 - golden hamster
C.Species: Mesocricetus auratus (golden hamster)
C.Date: 21-Sep.1993 #Sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C.Accession: B6233
C.Accession: M.S. #Mang. J. Chaddrick, R.B.; Rutter, W.J.
Ricerman, M.S. #Mang. J. Chaddrick, R.B.; Rutter, W.J.
Genes Dev 6 2165-2176 1992
A:71tle: Synergistic ectivation of the insulin gene by a LIM-homeo domain p
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A; Note:
                 A; Introns:
                                             A; Map position: 3
                                                                     A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                     A; Cross-references: EMBL: AL138648
                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <RIE>
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A;Cross-references: GB:X81406; ed:] Line HIT T-15 M.2 .2
A;Note: sequence extracted from NCBI backbone (NCBIN:117927, NCBIP:11792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-382 <GER>
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A:Accession: B46233
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Best Local
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Best Local
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5; Conserv
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5; Conserv
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Pred. No. 3.7e+02;
"" u'amatches 0;
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Pred. No. 3.8e+02;
1; Mismatches 0;
                                                                                             BAC clone F16M2
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Job time: 36 sec
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February

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2002, 08:00:52

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A;Molecule type: DNN
A;Residues; 1:384 <KUN
A;Cross-references: GB:299108; GB:ALO09126; NID:g2633055; PIDN:CAB12607.1; PID:e11827
A;Experimental source: strain 168
C;Genetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isech J.; Harwood, C.R.; Hensatt, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Konligstein, G.; Krogh, S.; Khanno, M.; Kurita, K.; Lapidus, A.; Lardino, R., Anuthors: Lauber, J.; Lazerevic, V.; Lee, S.M.; Lavine, A.; Liu, H.; Masuda, S.; Mau Y.; M.; Ogawa, K.; Ogiawar, A.; Ologab, B.; Rose, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl A.; Authors: Schleich, S.; Schroeter, R.; Scoftone, F.; Seklyuchi, J.; Sekowaka, A.; Scandakuchi, M.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; V.; Uchiya, T.; Miniers, P.; Mipat, A.; Yamanoto, H.; Yamanoto, K.; Yata, K.; Yata, K.; Yoshida, A.; H.; P.; Kata, K.; Yata, K.; Yoshida, A.; Tanakoshi, A.; Sekorome sequence of the Gram-positive bacterium Bacillus subtillinger; notelia, A.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores, M.; Millores,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spore germination protein homolog yfkR - Bacillus subtilis
C;Species; Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
                                                                                                                             Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
C.; Bron, S.; Broulliet, S.; Bsuschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmergon, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: D69809
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64 GGGTAG
                                                                             1 GGGTSG
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69
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                                                                                                                                                                                                          90.98;
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Pred. No.
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Pred. No. 3.8e+02;
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3.8e+02;
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Carter, N.M.;
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